U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office **SEARCH REQUEST FORM** Attiming Dilly Requestor's 68/938,548 Number: Name: Search Topic: Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s). Fleuse include an interference search. Thanks Pat STAFF USE ONLY Vendors Search Site STIC _ CM-1 STN Terminal time: _ Pre-S Dialog Elapsed time: APS Type of Search CPU time: Geninfo N.A. Sequence Total time: _ SDC A.A. Sequence Number of Searches: DARC/Questel Structure Number of Datagases:

Other

Bibliographic

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 12.09 Seconds 591.342 Million cell updates/sec

Fri Aug 20 20:53:06 1999; Run on:

Tabular output not generated.

>US-08-938-548B-2 (1-131) from US08938548B.pep 931 Description: Perfect Score:

1 MNLPSTKVSWAAVTLLLLLL......GRRCSAPAAASVAPGGQSGI 131 PAM 150 Gap 11 Scoring table:

Sequence:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_inammal 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 39.956; Variance 91.033; scale 0.439 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred. No	1.03e-14	5.14e-128	1.46e-1	2.72e-115	2.12e-02	1.60e-0	2.81e-0	3.71e-0]	1.12e+00	1.12e+00	1.12e+00	1.47e+00	1.47e+00	1.93e+0(1.93e+00	2.52e+00	3.29e+00	4.29e+00	5.58e+00	5.58e+00
Description	PREPRO-OREXIN.	PREPRO-OREXIN PRECURSO	PREPRO-OREXIN.	HYPOCRETIN (PREPRO-ORE	KIAA0634 PROTEIN (FRAG	HYPOTHETICAL 74.6 KD P	BAI 1.	POLYADENYLATE BINDING	NISHED (FRAGMENT).	GDNF FAMILY RECEPTOR A	MYB-LIKE DNA-BINDING D	HYPOTHETICAL 23.1 KD P	SODIUM DEPENDENT PHOSP	PROTEIN-TYROSINE PHOSP	KIAA0612 PROTEIN (FRAG	ORF469 PROTEIN.	SORTILIN PRECURSOR.	MRNA ENCODING RAMP2 PR	3' ORF.	ACYLOXYACYL HYDROLASE.
QI	043612	077668	055232	055241	075129	023352	014514	060455	042394	609090	049019	006319	087918	015255	075111	037839	099523	060895	061639	035298
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Query Match	100.0	8.06	84.0	83.2	11.8	11.1	10.8	10.7	10.3	10.3	10.3	10.2	10.2	10.1	10.1	10.0	o.	ø.	7.6	9.7
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131 AA.

PRT;

PRELIMINARY;

RESULT 2 ID 077668 AC 077668;

121 ASVAPGGOSGI 131 |||||||||||||||| 121 ASVAPGGOSGI 131

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5.5.58 ee+000 7.24 ee+000 9.3.88 ee+000 9.3.88 ee+000 9.3.88 ee+000 1.21 ee+000 1.21 ee+000 1.21 ee+000 1.22 ee+001 1.23 ee+001 1.24 ee+000 1.25 ee+001	PRIMATES; SON S., S., MA D.J., Ma D.J.,	Gaps 0; HA 60 H HA 60
LEUCINE_TICH REPEAT/RE LEUCINE_TICH REPEAT/RE FLT3 LIGAND, T169 FORM PRISTINAMYCIN I SYNTHA NOVEL SERINE PROTEASE. PHENOLOXIDASE (EC 1.10 TIGHT JUNCTION PROTEIN ANION EXCHANGER 2 A (F RIBOSOME RECEPTOR. MAV266 (FRAGMENT). HYPOTHETICAL 30.9 KD P BETA-(1-3)-GLUCOSYL TR VESICLE COAT PROTEIN S ORF PRECURSOR (FRAGMEN CTG4A. CTG4A. LEUCINE ZIPPER WITH BA F21B7.28. GLIAL GROWTH FACTOR 2 SEMAPHORIN B PRECURSOR ORF 24. ZK484.4 PROTEIN.	131 AA. UENCE UPDATE) DATION UPDATE) RATA; MAMMALIA; EUTHERIA; FSUZAKI I., CHEWELLI R.M., A.C., CARR S.A., ANIAN R. FISHOURBAGY N.A., BERGS 11y of hypothalamic neurop regulate feeding behavior	ngth 131; Indels 0; CSCRLYELLHGAGN
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
BUKARYOOTA; VIRIDIPLANATE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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BERGRAMP R., DIRKSE W., VAN STAVEREN M., STIEKEMA W., DROST L.,
RIDLEY P., HUDSON S.A., PATEL K., MURPHY G., PIFFANELLI P., WEDLER H.,
WEDLER E., WAMBUTT R., WEITZENEGGER T., POHL T.M., TERRYN N.,
GIELEN J., VILLARROEL R., DE CLERCK R., VAN MONTAGU M., LECHARNY A.,
AUBORG S., GY I., KREIS M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P.,
                                                                                                                                                                                                                                                                                     60 AGILTLGKRRPGPPGLQGRLQRLLQANGNHAAGILTMGRRAGAELEPHPCSGRGCPTVTT 119
                                                                                                                          1 MNFPSTKVPWAAVTLLLLLLL-PPALLSLGVDAQPLPDCCRQKTCSCRLYELLHGAGNHA 59
        Gaps
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DNA RES. 5:169-176(1998).

EMBL: AB014534; D1032570; -.

SEQUENCE 1321 AA: 145424 MW; 4B1721D3 CRC32;
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ISHIKAWA K., NAGASE T., SUYAMA M., MIYAJIMA N., TANAKA A., KOTANI
NOMURA N., OHARA O.;
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        Indels
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SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 74.6 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
13; Mismatches 10;
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Best Local Similarity 57.6%;
Matches 19; Conservative
    Conservative
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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107;
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075129;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
ENTIAN K.D., RIEGER M., SCHAEFEER M., FUNK B., MUELLER-AUER S.,
SILVEY M., JAMES R., MONTFORT A., PONS A., PUIGDOMENECH P., DOUKA A.,
VOUKELATOU B., MILIONI D., HATZOPOULOS P., PIRAVANDI E., OBERMAIER B.,
HILBERT H., DUESTERHOFT A., MOORES T., JONES J.D.G., ENEYA T.,
PALME K., BENES V., RECHMAN S., ANSORGE W., COOKE R., BERGER C.,
SCHUELLER C., CHALWATZIS N.;
"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
Arabidopsis thaliana.";
NATURE 391:485-488(1998).
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 KYCRSK-YETIHGQNHDNAADVLELAIKREMPAELL-R-ASLRHTNEDQRNFLLNVGRSA 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
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PEMBL; AB005297; DID24528; -.

PERML; PEO0090; tsp_l; 5.

SEQUENCE 1584 AA; 173531 MW; 235A5C42 CRC32;
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MEDLINE; 98208037.
CRAIG A.W.B., HAGHIGHAT A., YU A.T.K., SONENBERG N.;
"Interaction of polyadenylate-binding protein with the eIF4G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.8%; Score 101; DB 4; Length 1584; Best Local Similarity 50.0%; Pred. No. 2.81e-01; Matches 16; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                               / Match 11.1%; Score 103; DB 10; Length 679; Local Similarity 30.6%; Pred. No. 1.60e-01; es 19; Conservative 17; Mismatches 22; Indels
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NO-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYADENYLATE BINDING PROTEIN-INTERACTING PROTEIN-I
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                           679 AA; 74635 MW; B301B713 CRC32;
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Local Similarity 33.8%;
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les 14; Conservative
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CATARRHINI; HOMINIDAE; HOMO.
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(01-NOV-1996 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
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HOMO SAPIENS (HUMAN).
Gaps
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MEDLINE; 95086212.
HONDA H., INAZAWA J., NISHIDA J., YAZAKI Y., HIRAI H.;
HONDA H., INAZAWA J., NISHIDA J., YAZAKI Y., HIRAI H.;
HONDA H., INAZAWA J., NISHIDA J., YAZAKI Y., HIRAI H.;
HONDA H., INAZAWA J., NISHIDA J., YAZAKI Y., HIRAI H.;
BLODO 84:4166-4194(1994).
BLODO 84:4166-4194(1994).
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS0041: fn3: 5.
PFAM; PF00102; Y_Dhosphatase; 1.
SIGNAL; GLYCOPROFEIN; TRANSMEMBRANE; REPEAT; HYDROLASE.
SIGNAL; GLYCOPROFEIN; TRANSMEMBRANE; REPEAT; HYDROLASE.
                                                                                                                                                                                                                                                                                                     [1] SECONONCE FROM N.A.
STRAIN—51569;
LEBENS M., SODERLUND L.O., LUNDQUIST P., CARLIN N.I.A.;
LEBENS M., SODERLUND L.O., LUNDQUIST P., CARLIN N.I.A.;
"A putative sodium dependent phosphate pump in Vibrio cholerae.";
SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, A010968, E1322408; -.
SFOUENCE 382 AA; 40223 MW; 62A54A68 CRC32;
                                                                                                                                                                                                                                                                                        BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
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LAST ANNOTATION UPDATE)
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                                                154 AADDHIAAIALFGNPSG 170
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|86 ASGNHAAGILTMGRRAG 102
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EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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ISHIKAWA K., NAGASE T., SUYAMA M., MIYAJIMA N., TANAKA A., KOTANI H., NOMUKA N., OHARA O.;
"Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA RES. 5:169-176(1998).
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Pred. No. 1.93e+00;
13; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1337;
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01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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NON_TER 1 1 SEQUENCE 1736 AA; 187040 MW; 95603A22 CRC32;
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Pred. No. 1.93e+00;
7; Mismatches 6
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(TM)	*****

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 20:52:28 1999; MasPar time 5.99 Seconds 618.331 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-2 (1-131) from USO8938548B.pep 931 Title:

1 MNLPSTKVSWAAVTLLLLLL......GRRCSAPAAASVAPGGQSGI 131 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

77977 seqs, 28268293 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

Mean 41.738; Variance 80.369; scale 0.519 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	5.06e-03 5.06e-03 7.09e-02 7.56e-02 7.56e-02 1.04e-01 1.42e-
Description	PROSTAGIANDIN G/H SYNT SECRETIN PRECURSOR (FR HYPOTHETICAL 38.7 KD P TENSIN. PROSTAGIANDIN G/H SYNT PROTEIN-TYROSINE PHOSP PROTEIN-TYROSINE PHOSP ADBNYLATE CYCLASE, TYP URIDINE KINASE (EC 2.7 PROCHETICAL 22.7 KD FROTEIN HYPOTHETICAL 22.7 KD FROTEIN K PROTHETICAL PROTEIN K PROTEIN-TYROSINE PHOSP CATION-INDEPENDENT MAN RETINAL GUANYLYL CYCLA SL CYTOKINE PRECURSOR COMPLEMENT CIQ SUBCOMP SEX HORMONE-BINDING GL TRANS-ACTING TRANSCRIP TRANS-ACTING TRANSCRIP STROMELYSIN-3 PRECURSOR STROMELYSIN-3 PRECURSOR STROMELYSIN-3 PRECURSOR
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DB	еспенинананананана
Length	602 1311 1312 1313 1013 1013 1016 1016 1017 1010 1010 1010 1010 1010
% Query Match	111111 1111111 11111111111111111111111
Score	00000 00000 00000 00000 00000 00000 0000
Result No.	10 8 4 8 9 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

1.62e+00 1.62e+00 1.62e+00	1.62e+00 1.62e+00 1.62e+00 2.17e+00	2.17e+00 2.17e+00 2.17e+00	2.90e+00 2.90e+00 2.90e+00	2.90e+00 2.90e+00 2.90e+00	3.87e+00 3.87e+00	3.87e+00
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75 75 75 75 75	308	337	3 3 3 4 3 6 5 7	38 40 41 11	44 44 44	45

ALIGNMENTS

SULT 1 PGH1_RAT STANDAF Q63921; Q62731; Q63684			STRA STRA MEDL KITZ ANA PGHS ARCH	CC CELLS. CC -!- CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) = PROSTAGLANDIN H2 + A + H(2)0. CC -!- PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND CC -!- SUBGOXANES. CC -!- SUBGOXANES. CC -!- SUBGOXANES. CC -!- SUBGOXANES. CC -!- THIS BNIZME ACTS DOTH AS A DIOXYGENASE AND AS A PERCYLOAR DOTH AS A DIOXYGENASE AND AS A PERCYLOAR DOTH AS A DIOXYGENASE AND AS A PERCYLOAR DOTH AS A DIOXYGENASE.	SUCH AS ASPIRIN -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. -!- SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY
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01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
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CONFLICT
CONFLICT
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL 38.7 KD PROTEIN IN TKTB-NARQ INTERGENIC REGION PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LLFFFALLPTSLVWAAPAQRAFSD--WQVTCNNQNFCVARNTGDHNGLVMTLSRSAGAHT 64
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BLATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y., The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
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                                    18
56 SECRETIN.
56 AMIDATION (G-57 PROVIDE AMIDE GROUP).
14277 MW, 837D201A CRC32;
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ESCHERICHIA.
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                                                                                          Length 131;
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                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 HYPOTHETICAL PROTEIN YPFG. 38746 MW; 136C8304 CRC32;
                                                                                        Score 107; DB 1;
Pred. No. 5.66e-03;
                                                                                                             Mismatches
PFAM; PF00123; hormone2; 1.
HSSP; P01274; 1GCN.
GLUCAGON FAMILY; HORMONE; AMIDATION; SIGNAL.
                                                                                                                                                                                          347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TENS_CHICK STANDARD; PRT; 1744 AA Q04205; Q91007; Q92011; 01-NOV-1995 (REL. 32, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                         PRT;
                                                                                                                                24
                                                                                                                                                  16 LLLLLLPPALLSSGAAAQPLP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECOGENE; EG14194; YPFG. HYPOTHETICAL PROTEIN; SIGNAL.
                                                                             3 LLLLLLLPPLLLLAGCAARPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000333; G1788809; -
                                                                                         11.5%;
72.7%;
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 347 AA;
                                                                    131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 DAVLRIER 72
                                                                                                                                                                                                                                                            ESCHERICHIA COLI
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56
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YPFG_ECOLI
P76559;
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                                                                     SEQUENCE
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MOD_RES
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SIGNAL
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MEDLINE: 91220073.

A REDLINE: 91220073.

A ROBERTS T.M., AN Q., CHEN L.B.;

R POBERTS T.M., AN Q., CHEN L.B.;

R PERSENCE Of an SH2 domain in the actin-binding protein tensin.";

U. SCIENCE 252:712-715(1991).

C -1- FUNCTION: MAY BE INVOLVED IN CELL MIGRATION, CARTILAGE DEVELOPMENT

AND IN LINKING SIGNAL TRANSDUCTION PATHWAYS TO THE CYTOSKELETON.

BINDS TO ACTINS AND PHOSPHORYLATED PROTEINS IN SRC-TRANSFORMED

CELLS. MAY BIND ACTIN WITH CAPPING AND BUNDLING PROPERTIES:

C -1- SUBCELLULAR LOCATION: LOCALIZES TO ADHERENS JUNCTIONS.

C -1- TISSUE SPECIFICITY: HEAPT, GIZZARD, LUNG AND SKELETAL MUSCLE.

C -1- PTM: TYROSINE-PHOSPHORYLATED.

C -1- SIMILARITY: CONTAINS A TENSIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              LO S.H., AN Q., BAO S., WONG W.K., LIU Y., JANMEY P.A., HARTWIG J.H.,
                                                                                                                                                                                                                                                                                                                              "Molecular cloning of chick cardiac muscle tensin. Full-length cDNA sequence, expression, and characterization.";
J. BIOL. CHEM. 269:22310-22319(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAN DE WERKEN R., GENNARI M., TAVELLA S., BET P., MOLINA F., LIN S., CANCEDDA R., CASTAGNOLA P.; Modulation of tensin and vimentin expression in chick embryo developing cartilage and cultured differentiating chondrocytes."; EUR. J. BIOCHEM. 217:781-790(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95204530.
CHUANG J.Z., LIN D.C., LIN S.;
Molecular cloning, expression, and mapping of the high affinity actin-capping domain of chicken cardiac tensin.";
J. CELL BIOL. 128:1095-1109(1995).
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SH2 DOMAIN; PHOSPHORYLATION. TENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (XXX-1991) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=EMBRYONIC CHONDROCYTES, AND EMBRYONIC HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH2.
C -> R (IN REF. 2).
M -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, M96625, G619577; -.
EMBL, L06662, G212755; ALT_INIT.
EMBL, 218529, G63805; ALT_INIT.
EMBL, M74165, G212752; -.
EMBL, X66286; G63803; -.
PROSITE: PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1469-1744 FROM
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HSSP; P16277; 1BLJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94039118.
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                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     MEDLINE; 94350987
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                                                  Gaps
                                                                                                                                                                     01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONSECUTIVE BASIC RESIDUES (BY SIMILARITY).
SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
                                                                                                                                                                                                                                              MACACA NEMESTRINA (PIG-TAILED MACAQUE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GASTROINTESTINAL TRACT.
PTM: APPEARS TO UNDERGO MULTIPLE PROTEOLYTIC CLEAVAGE AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN-TYROSINE PHOSPHATASE X. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE SITE (BY SIMILARITY)
                       Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHATASE
                     Score 101; DB 1; Length 599
Pred. No. 4.00e-02;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROLASE; RECEPTOR; GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9EC7D263 CRC32;
68656 MW; 8C7684CD CRC32;
                                                                                                                                                 PRT; 1013 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U91574; G1916942; -.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
PFAM: PF00102; Y_phosphatase; 1.
HSSP; P18052; 1YFO.
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                                                                                    10 LLFLLLLPPLPVLLADPGAPTPVNPCC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111190 MW;
                     Query Match 10.8%;
Best Local Similarity 51.9%;
Matches 14; Conservative
                                                                                                                                               STANDARD;
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1013
1002
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562 56
1013 AA;
599 AA;
                                                                                                                                   T 6
PTPX_MACNE
SEQUENCE
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ACT_SITE
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CARBOHYD
                      Query Match
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DOMAIN
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DB 1; Length 1013;

Score 99;

10.6%;

Query Match

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILNE; 97032784.

KAWASAKI E., HUTION J.C., EISENBARTH G.S.;

"Molecular cloning and characterization of the human transmembrane protein tyrosine phosphatase homologue, phogrin, an autoantigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PANCREATIC ENDOCRINE CELLS. OPTIMUM ACTIVITY IS MEASURED AT PH
                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN)
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-!- DISEASE: AUTOANTIGEN IN INSULIN-DEPENDENT DIABETES MELLITUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN TYROSINE + ORTHOPHOSPHATE.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).

-!- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND PANCREAS.

LEVELS IN TRACHEA, PROSTATE, STOMACH AND STINAL CHORD.

-!- PTM: APPEARS TO UNDERGO MULTIPLE PROTEOLYTIC CLEAVAGE AT
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EURARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRINATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONSECUTIVE BASIC RESIDUES.
DOMAIN: THE CYTOPLASMIC DOMAIN APPEARS TO CONTAIN THE
                                 Indels
Best Local Similarity 57.1%; Pred. No. 7.56e-02;
Matches 12; Conservative 7; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOCHEM. BIOPHYS. RES. COMMUN. 227:440-447(1996)
                                                                                                                                                                                                                       | TESULT | 7 | STANDARD; | PRT; | LULD | CLUD | CLU
                                                                                         56
                                                                                                                                                35
                                                                                                                       EMBL; U66702; G1620664; -. EMBL; Y08569; E273864; -. EMBL; AF007555; G2262075; ..
                                                                                         6 LLLLLLLPPRVLPAAPSSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=FETAL BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-PANCREAS;
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YKO7_YEAST
P36061;
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P09340;
 CHAIN
DOMAIN
ACT_SITE
ACT_SITE
                                                               MOD_RES
DISULFID
                                                                                                                  DISULFID
                                                                                          DISULFID
                                                                                                       DISULFID
                                                                                                                                              CARBOHYD
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                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                  SEQUENCE
                                                     BINDING
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                      01-AUG'1991 (REL. 19, CREATED)
01-AUG'1991 (REL. 19, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANDOTATION UPDATE)
PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE
-1) (COX-1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1) (PROSTAGLANDIN H2
SXNTHASE 1) (PRH SYNTHASE 1) (PGHS-1) (PHS 1).
PTG31 OR COX1 OR COX-1.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 90203007.

DEWITT D.L., EL-HARITH E.A., KRAEMER S.A., ANDREWS M.J., YAO E.F., ARMSITOONG R.L., SMITH W.L.;

The aspirin and heme-binding sites of ovine and murine prostaglandin endoperoxide synthases.";

J. BIOL. CHEM. 265:5192-5198(1990).

-!-FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING OR PROMOTING CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE. THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE. THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS SUCH AS ASPIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) = PROSTAGLANDIN
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OXIDOREDUCTASE; DIOXYGENASE; PEROXIDASE; GLYCOPROTEIN; ACETYLATION; PROSTAGLANDIN BIOSYNTHESIS; HEME; IRON; SIGNAL; MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \mathrm{H2} + \mathrm{A} + \mathrm{H(2)O}. PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                           Pred. No. 1.42e-01;
14; Mismatches 13; Indels
                                                                                                                 Length 260;
                                                                                                                                                                   218 LCKRHRGGPNGRNH-KRTFPEPGDHP-GVLATGKRSHLESSSRP 259
                                                                                                                                                                                  1
260 AA; 29622 MW; E72BB622 CRC32;
                                                                                                                                                                                                                                                 602 AA.
                                                                                                                  Score 97;
                                                                                                                                                                                                                                                 PRT;
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                                                                                                                 Query Match

Best Local Similarity 34.18;
                                                                                                                                           15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M34141; G200303; -.
                                   EMBL; L31783; G471981; -.
MGD; MGI:98904; UMPK.
TRANSFERASE; KINASE.
                                                                                                                                                                                                                                                 STANDARD;
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MGD; MGI:97797; PTGS1
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PGH1_MOUSE
P22437;
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SEQUENCE
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                                       DISTAL HISTIDINE (BY SIMILARITY).
CYCLOOXYGENASE (BY SIMILARITY).
PROXIMAL HEME LIGAND (BY SIMILARITY).
ASPTRIN-ACETYLATED SERINE.
BY SIMILARITY.
BY SIMILARITY.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKL147C OR YKL601.
SACCHAROWYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (REL. 29, CREATED)
1-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST SHORDATION UPDATE)
HYPOTHETICAL 22.7 KD PROTEIN IN SDH1-CIM5/YTA3 INTERGENIC REGION
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PROSTAGLANDIN G/H SYNTHASE 1.
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Pred. No. 1.94e-01;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB 1; Length 602;
Pred. No. 1.42e-01;
7; Mismatches 12; Indels
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PIR; S44581, S44581.
SEQUENCE 205 AA; 22673 MW; OAEA8D4E CRC32;
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96489281 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 WFPLLLLLLLPPTPSVLLADPGVPSPVNPCC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                          146 E
69042 MW;
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Best Local Similarity 38.7%;
Matches 12; Conservative
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Best Local Similarity 53.8%;
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MEDLINE; 94378720.
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JOBEL P., DAHMS N.M., BREITMEYER J., CHIRGWIN J.M.,
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01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (CI MAN-6-P
RECEPTOR) (CI-MPR) (INSULIN-LIKE GROWTH FACTOR II RECEPTOR).
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE: 88115411.
LOBEL P., DAHMS N.M., KORNFELD S.;
Cloning and sequence analysis of the cation-independent mannose 6-phosphate receptor.";
J. BIOL. CHEM. 263:2563-2570(1988).
                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                 BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ĀRTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                   Score 94; DB 1; Length 1337;
Pred. No. 3.59e-01;
                                                                                                                                                                                                                                                POTENTIAL.
W; 55F90A6B CRC32;
                               BY SIMILARITY.
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SEQUENCE OF 1039-2499 FROM N.A.
MEDLINE; 87175648.
                                                                                                                                                                                                                                                       145985
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14; Conservative
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SEQUENCE FROM N.A.
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                                                  PROC. NATL. ACAD. SCI. U.S.A. 84:2233-2237(1987).

- I- FUNCTION: TRANSPORT OF PHOSPHORYLANDED LINSOSOMAL ENZYMES FROM
THE GOLGI COMPLEX AND THE CELL. SURFACE TO LINSOSOMES. LINSOSOMAL
ENZYMES BEARING PHOSPHOMANNOSYL RESIDUES BIND SPECIFICALLY TO
MANNOSE-6-PHOSPHATE RECEPTORS IN THE GOLGI APPARATUS AND THE
RESULTING RECEPTOR-LIGAND COMPLEX IS TRANSPORTED TO AN ACIDIC
PRELYOSOMAL COMPARTMENT WHERE THE LOW PH MEDIATES THE DISSOCIATION
OF THE COMPLEX. THIS RECEPTOR ALSO BINDS INSULIN GROWTH FACTOR II.

-! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. LISSOSOMAL.

-! DOMAIN: CONTAINS 15 REPEATING UNITS OF APPROXIMATIVELY 147 AA. THE
MOST HIGHLY CONSERVED REGION WITHIN THE REPEAT CONSISTS OF A

STRETCH OF 13 AA THAT CONTAINS CYSTEINES AT BOTH ENDS.
                              'Cloning of the bovine 215-kDa cation-independent mannose 6-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. . CATION-INDEPENDENT MANNOSE-6-PHOSPHATE
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KORNFELD S.
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PIR; A30788; A30788.
PROSITE; PS00023; FIBRONECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00040; fn2; 1.
PFAM; PF00878; CIMR_repeat; 12.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 20:51:49 1999; MasPar time 8.66 Seconds 606.456 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-2 (1-131) from USO8938548B.pep 931 1 MNLPSTKVSWAAVTLLLLLL......GRRCSAPAASVAPGGQSGI 131

Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Post-processing:

Searched:

Minimum Match 0% Listing first 45 summaries

1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 40.416; Variance 87.828; scale 0.460 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	9.52e-03	1.29e-02	1.75e-02	2.36e-02	2.36e-02	4.29e-02	7.76e-02	7.76e-02	1.04e-01	1.04e-01	1.39e-01	1.39e-01	1.39e-01	2.49e-01	2.49e-01	2.49e-01	3.32e-01	4.41e-01	5.86e-01	5.86e-01	7.77e-01	7.77e-01	1.03e+00
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100382 #type fragment hypothetical protein KIAA0634 - human (fragment) #formal_name Homo sapiens #common_name man 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999		Ishlkawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.	ınidenti	genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.		preliminary; translated from GB/EMBL/DDBJ			##cross-references EMBL:AB014534; NID:d1204289; PID:d1032570 ##exnerimental course brain				Score 110; DB 2; Length 1321;	7; Mismatches 4; Indels
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음 δ S69198 #type complete
prostaglandin G/H synthase 1 - rat
#formal_name Rattus norvegicus #common_name Norway rat
24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change
10-Sep-1997
s60109, Kitzler, J.W. submitted to the EMBL Data Library, December 1994 S69198 S69198 #submission #accession ##status #authors ACCESSIONS REFERENCE RESULT ENTRY TITLE ORGANISM DATE

##molecule_type mRNA ##residues 1-602 ##label KIT preliminary

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Analysis of 1.9 Mb of contiguous sequence from chromosome 4
                                                                                                 translation not shown
                 of Arabidopsis thaliana. #cross-references MUID:98121113
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Dean, C.; Bergkamp, R.; Dirkse, W.; Van Staveren, M.;
Stiekema, W.; Drost, L.; Riddey, P.; Hudson, S.A.; Patel,
K.; Murphy, G.; Piffanelli, P.; Wedler, H.; Wedler, E.;
Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.;
Gielen, J.; Villarroel, R.; De Clerck, R.; Van Montagu, M.;
Lecharny, A.; Auborg, S.; Gy, I.; Kreis, M.; Lao, N.;
Kavanaqh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger,
M.; Schaeffer, M.; Funk, B.; Mueller-Auer, S.; Silvey, M.;
James, R.; Montfort, A.; Pons, A.; Puigdomenech, P.; Douka,
A.; Voukelatou, E.; Milioni, D.; Hatzopoulos, P.;
Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.;
Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.;
Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny,
M.; Voet, M.; Volckaert, G.; Mewes, H.W.; Klosterman, S.;
Schueller, C.; Chalwatzis, N.
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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hypothetical protein b2466 - Escherichia coli (strain K-12)
#formal_name Escherichia coli
12-sep.1997 #sequence_revision 17-Sep-1997 #text_change
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hypothetical protein - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
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(Y #length 347 #molecular-weight 38746 #checksum 7897
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#journal J. Cell Biol. (1995) 128:1095-1109
#title Molecular cloning, expression, and mapping of the high
affinity actin-capping domain of chicken cardiac tensin.
#cross-references MUID:95204530
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                                                                ##residues 1-679 ##label BEV ##cross-references GB:297337; NID:92244829; PID:e326841; PID:92244855
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Pred. No. 7.76e-02;
13; Mismatches 22; Indels 4; Gaps
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#formal_name Gallus gallus #common_name chicken
05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change
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MARX #length 679 #molecular-weight 74635 #checksum 9028
nucleic acid sequence not shown
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FICATION #superfamily SH2 homology
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17; Mismatches 22;
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                                                                                                                                                                                                                      #Journal Diaz, A.; Reginato, A.M.; Jimenez, S.A.
#journal J. Biol. Chem. (1992) 267:10816-10822
#title Alternative splicing of human prostaglandin G/H synthase mRNA and evidence of differential regulation of the resulting transcripts by transforming growth factor beta 1, interleukin 1 beta, and tumor necrosis factor alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214064
Nishimori, H.; Shiratsuchi, T.; Urano, T.; Kimura, Y.;
Kiyono, K.; Tatsumi, K.; Yoshida, S.; Ono, M.; Kuwano, M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barnett, J.; Chow, J.; Ives, D.; Chiou, M.; Mackenzie, R.; Osen, E.; Nguyen, B.; Tsing, S.; Bach, C.; Freire, J.; Chan, H.; Sigal, E.; Ramesha, C. C.; Freire, J.; Chor, H.; Sigal, E.; Ramesha, C. C.; Freire, J.; Colim. Biophys. Acta (1994) 1209:130-139
Purification, characterization and selective inhibition of human prostaglandin G/H synthase 1 and 2 expressed in the
                              #domain signal sequence #status predicted #label SIGN #product prostaglandin-endoperoxide synthase #status experimental #label MAT #are #status #length 599 #molecular-weight 68656 #checksum 4138
                                                                                                                                                                                                                                                                                                                                                                                   This enzyme is bifunctional with the fatty acid cyclooxygenase activity and prostaglandin hydroperoxidase activity.
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22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change
12-Feb-1999
                Funk, C.D.; Funk, L.B.; Kennedy, M.E.; Pong, A.S.;
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BAI1 protein
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Pred. No. 1.39e-01;
                                                                                                                                                                     ##cross-references GDB:128070; OMIM:176805
#map_position 9q32-9q33.3
WORDS alternative splicing; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #type complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type protein
##residues 24-32 ##label BAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    baculovirus system.
#cross-references MUID:95035046
                                                                                                        assignment.
#Cross-references MUID:91317397
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Best Local Similarity 51.9%;
Matches 14; Conservative
                                                                                                                                                       ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
##residues 1-599
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A39937
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ORGANISM
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                  #authors
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24-599
REFERENCE
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                                                                                                                                                                                                                                    #domain thrombospondin type 1 repeat homology #label
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the authors translated the codon AGT for residue 25
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protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type
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                                                                                                                                                                             #map_position 8q24-8q24
CLASSIFICATION #superfamily thrombospondin type 1 repeat homology
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                                                                    ##residues 1-1584 ##label NIS ##cross-references EMBL:AB005297; NID:d1175078; PID:d1024528
                                                                                                                                                                                                                                                                                                          Length 1584;
submitted to the EMBL Data Library, June 1997 T00026
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Pred. No. 2.49e-01;
9; Mismatches 2; Indels
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31-Jan-1997 #sequence_revision 31-Jan-1997
13-Nov-1998
                                                                                                                                                                                                                                                       THR3
#length 1584 #molecular-weight 173531
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                                                                                                                                                                                                                                                                                                        Score 101; DB 2;
Pred. No. 1.39e-01;
                                    ranslated from GB/EMBL/DDBJ
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##cross-references GDB:9838088; OMIM:602682
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                                                                                                                                                                                                                                                                                                                                                                                12 WILAPLLLLLLLGRRARAAGADAGPGPEPC 43
                                                                                                                                                                                                                                                                                                                                                                                                                  10 WAAVTLLLLLLL-PPALLSSGAAAQPLPDCC 40
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                                                                                                         ##experimental_source brain
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Best Local Similarity 47.6%;
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0%;
Matches 16; Conservative
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##residues 1-24
                                                     ##molecule_type mRNA
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MasPar time 6.37 Seconds 239.851 Million cell updates/sec Fri Aug 20 20:58:15 1999; Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Tabular output not generated.

>US-08-938-548B-4 (1-18) from US08938548B.pep 196 1 RSGPPGLQGRLQASGNHAAGILIM 28 Title:

Description: Perfect Score: Sequence: PAM 150 Gap 15 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 30.076; Variance 50.517; scale 0.595 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.42e-25	ECURSO 6.55e-25	RO-ORE 3.01e-24	m	ROTEIN 2.25e-01	1.45e+00	SUBUN 2.09e+00	PROTEI 2.09e+00	3.00e+00	3.00e+00	3.00e+00	IGMA-L 4.29e+00	4.29e+00	6 KD P 4.29e+00	4	. 6.12e+00	IGMA-L 6.12e+00	ZOYL-C 6.12e+00	SIGMA F 6.12e+00	SIGMA F 6.12e+00
Description	PREPRO-OREXIN.	PREPRO-OREXIN PRECURSO	HYPOCRETIN (PREPRO-ORE	PREPRO-OREXIN.	TIGHT JUNCTION PROTEIN	T13D8.6 PROTEIN.	K+ CHANNEL BETA4 SUBUN	PAR INTERACTING PROTEI	HRPE.	ARTICULIN P60.	H06001.2 PROTEIN	RNA POLYMERASE SIGMA-L	YONC PROTEIN.	HYPOTHETICAL 19.6 KD P	RETINOID X RECEPTOR IN	T9J22.21 PROTEIN	RNA POLYMERASE SIGMA-L	D-SUBUNIT OF BENZOYL-C	RNA POLYMERASE SI	RNA POLYMERASE SI
GI .	043612	077668	055241	055232	095168	080740	P97382	035821	052495	027212	017909	085680	031955	064066	060811	048721	085683	087877	P95644	059913
BB :	4	9	11	11	9	10	11	11	7	Ŋ	Ŋ	7	7	σ	Ξ	10	7	~	7	7
Query Match Length DB	131	131	130	130	1174	511	249	1277	439	268	1465	162	178	178	580	145	161	282	462	210
Query Match	100.0	98.5	96.9	6.96	38.8	36.2	35.7	35.7	35.2	35.2	35.2	34.7	34.7	34.7	34.7	34.2	34.2	34.2	34.2	34.2
Score	196	193	190	190	97	71	70	70	69	69	69	68	68	89	89	67	67	67	67	67
Result No.	-	7	ю	4	S	9	7	6 0	თ	10	11	12	13	14	15	16	17	18	19	20

6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	6.12e+00	8.69e+00	8.69e+00	8.69e+00	8.69e+00	8.69e+00	1.23e+01	1.23e+01	1.23e + 01	1.23e+01	1.23e+01	1.23e+01	1.23e + 01	1.73e+01	1.73e + 01
MAJOR VEGETATIVE SIGMA	RNA POLYMERASE SIGMA F	RNA POLYMERASE SIGMA F	RNA POLYMERASE SIGMA F	HYPOTHETICAL 60.1 KD P	POLYPROTEIN.	VP2, NS, VP3.	PUTATIVE ABC TRANSPORT	TYLACTONE SYNTHASE MOD	NUMA PROTEIN.	PRISTINAMYCIN I SYNTHA	TNA2, TNA1, PARTIAL AN	LEUCINE ZIPPER WITH BA	STEROID 21-HYDROXYLASE	KIAA0566 PROTEIN (FRAG	P160 MYB-BINDING PROTE	MOUSE 57-KD CALCIUM-BI	HYPOTHETICAL 33.8 KD P	3-HYDROXYISOBUTYRYL-CO	TRANSCRIPTIONAL ACTIVA	F14D7.2 PROTEIN.	HYPOTHETICAL 55.5 KD P	OXOGLUTARATE DEHYDROGE	ORF263.	HSGAK.
050539	P77951	059813	059814	069851	P89521	055651	081016	033958	Q14980	054959	050648	091640	054797	060312	035851	062041	033744	092931	050205	019452	042651	049541	931722	014976
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29	29	67	67	67	67	29	67	29	67	67	99	99	99	99	99	65	65	65	65	. 69	65	65	64	64
21	22			25		27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

1 PRELIMINARY; PRT; 131 AA. 043612; 043612; 01-JUN-1998 (TREMBLREL. 06, CREATED) 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) 01-MOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION S., NATSOLNOES FROM N.A., NOSLOWERS (G.P., WILSON S., ARCH J. N.S., EUCKINCHAM R.E., HAVINES A.C., CARR S.A., ANNAN R.S., MCNULTY D.E., LIU WS., TERRETT J.A., ELSHOURBAGY N.A., BERGSMA D.J., YANAGISANA M.; 07 EXAINS AND O'S TREATED TO A., NOSLOWENCE N.A., BERGSMA D.J., TANKA M. S., ANDOTATION S., AND S., ANDOTATION S., AND S.,
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Pred. No. 1.42e-25; 0; Mismatches 0; Indels Best Local Similarity 100.0%; Matches 28; Conservative

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Gaps

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23
                                                  1 RSGPPGLQGRLQRLLQASGNHAA
                                   308 QSTPPGLQARAGRLVAAKSTLAA
                                                                                             RESULT 7
1D P97382,
AC P97382,
DT 01-MAY-1997 (TREMBLREL. 03,
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Best Local Similarity 25.9%;
Matches 7; Conservative
 Best Local Similarity 52.2%;
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Similarity 81.8%;
9; Conservative
             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACERE; ARABIDOPSIS.
                                                       BEATCH M., JESAITIS L.A., GALLIN W., GOODENOUGH D.A., STEVENSON B.R.; "The tight junction protein ZO-2 contains three PDZ (PSD-95/Discs-Large/ZO-1) domains and an alternatively spliced region."; J. BIOL. CHEM. 271:25723-25726(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA.
VISOTSKAIA V.S., SCHWARTZ J.R., KWAN A., TORIUMI M., YU G., OJI, O,
LIU S., LI J., ARAUJO R., AU M., BRENDEL V., BUBHLER E., CONWAY A.B.,
CONWAY A.R., DEWAR K., FENG J., KIM C., KURTZ D., LI Y., PALM C.J.,
SHINN P., SUN H., DAVIS R.W., ECKER J.R., FEDERSPIEL N.A.,
THEOLOGIS A.,
"Arabidopsis thaliana chromosome 1 BAC T13D8 sequence.";
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                            Length 1174;
                                                                                                                                                                                                                                                                         Query Match 38.8%; Score 76; DB 6; Length 1174 Best Local Similarity 35.7%; Pred. No. 2.25e-01; Matches 10; Conservative 10; Mismatches 8; Indels
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SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
BUBL; 1.27152; G1556970; -.
PFAM; PRO0595; PDZ; 3.
PFAM; PF00625; Guanylate, Kin; 1.
SEQUENCE 1174 AA; 132085 MW; 2FA16B83 CRC32;
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SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                           GOODENOUGH D.A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                511 AA
                                                                                                                                                                                                                                                                                                                        268 RSPSPELRGRPDHAGQPDSDRPIGVLLM 295
                                                                                                                                                                                                                                                                                                                                     CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
 Nor suppressor protein.";
CELL BIOL. 124:949-961(1994).
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08,
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SEQUENCE 511 AA; 55547
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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STRAIN=CV. COLUMBIA;
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THEOLOGIS A.;
                                 SEQUENCE FROM N.A. MEDLINE; 96421547.
                                                                                                                               SEQUENCE FROM N.A.
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Length 511;

DB 10;

36.2%; Score 71;

Query Match

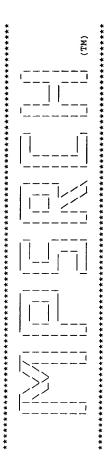
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MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MUSINAE; MUS.
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EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
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WUMARIN J., SCHIBLER U.;
"Expression of the liver-enriched transcriptional activator protein
DBP follows a stringent circadian rhythm.";
CELL 63:1257-1266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FINK M., DUPRAT F., LESAGE F., HEURTEAUX C., ROMEY G., BARHANIN J., LAZDUNSKI M.;
"A new K+ channel beta subunit to specifically enhance Kv2.2 (CDRK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                      Indels
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SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U83590; G2253211; -
SEQUENCE 1277 AA; 144674 MW; 89721F79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                           01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
Pred. No. 1.45e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 11; 1 Pred. No. 2.09e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70; DB 11; 1 Pred. No. 2.09e+00;
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05, LAST SEQU
08, LAST ANNO
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EMBL; U65593; G1695272; -.
IONIC CHANNEL.
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AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORGISER L., BRANS A., BRANN M., BRIGHELL S.C., BRON S.,
BROUILLET S., BOURELLER L., BRANS A., BRANN M.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
BROUILLET S., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA BENTION K.D., ERRINGTON J., FEBRET C., FOULGER D.,
RAILLER M., FUJITA M., FUJITA Y., FUMA S., GALICETI E., FOULGER D.,
ALLEBET H., HOLSAPPEL S., HOSONO S., HOLLO M.F., ITAYA M., JONES L.,
ACUISEPPI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENAUT A.,
JORIS B., KRRAMATA D., KASHARA Y., KLAERR BLANCHARD M., KLEIN C.,
ACUISEPPI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENDIOUS A.,
AURITA K., LEVINE A., LARDINOIS S., LAUBER J., LAZARENIC C.,
ANDRIAN K., LEVINE A., LIN MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
ANDONE D., O'RELLLY M., PORTEFELLE D., PORMOLLIK S., PRESCOTT A.M.,
PARRO V., POHL T.M., PORTEFELLE B., RADORNIC G., REY M., REYNOLDS S.,
ANDRESCAN E., PULIC P., PURNELLE B., RADORNE F.,
ANDRESCAN E., PULIC P., PURNELLE B., RADORNE F.,
ANDRESCAN E., SCHELCH S., SCHEDER R., SALDAIE F.,
ANDRESCAN E., SCHELCH S., SCHEDER R., SALDAIE F.,
ANDRESCAN E., SCHELCH S., SCHEDER R., SCHEDENE F.,
ANDRIAN N., MANBUTT R., WEDLER H., VASSAROTTI A.,
ANDRIES P., WIRMA A., YANDENBOL M., VANDENRE T.,
ANDRIES P., WIRMA A., YANDENBOL M., VANDEN R., WASHING R., YASHING R.,
ANDRIES P., WIRMA A., YANDENBOL M., VASSINOTO K., YATA R.,
ANDRIES P., WIRMA A., YANDENBOL M., VASSINOTO K., YATA R.,
ANDRIES P., WIRMA A., YANDENBOL M., VANDER R., WASHING R., YOSHIDA R., YOSHIRAWA H., DANCHIN A., THE COMPLETE WE WENCH THE STANDARD M., WINTERS P., WIRMA A., YANDENBOL M., VANDENBOL M., VANDENBO
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BACILLUS.
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                                                                                                                                                Score 68; DB 2; Length 162;
Pred. No. 4.29e+00;
10; Mismatches 4; Indels
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Pred. No. 4.29e+00;
4; Mismatches 7; Indels
                                                                                                                                                                                            4; Indels
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SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 299115; E1183561; -
SEQUENCE 178 AA; 19609 MW; CA7BBEDO CRC12.
                                                                                                                                                                                                                                                                                                                                                                                                                                    LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                        162 AA; 18499 MW; 633A3527 CRC32;
                                                                                                                                                                                                                                                                                                                                                                        178 AA
from Actinomycetes.";
J. MICROBIOL. BIOTECHNOL. 8:280-283(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                       111 LODQLQQVLQTLSEREAGVVRL 132
                                                                                                                                                                                                                                                               7 LOGRLDARLDASGNHAAGILIM 28
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01-JAN-1998 (TREMBLREL. 05,
01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                              Query Match 34.7%;
Best Local Similarity 36.4%;
Matches 8; Conservative
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Best Local Similarity 45.0%;
Matches 9; Conservative
                                     EMBL; AF071792; G3249723;
NON_TER 1 1
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                                                                                    162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS SUBTILIS.
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MEDLINE; 98044033
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SEQUENCE
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MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95280959.
SEOL W., CHOI H.S., MOORE D.D.;
SEOL W., CHOI H.S., MOORE D.D.;
"Isolation of proteins that interact specifically with the retinoid X receptor: two novel orphan receptors.";
MOL. ENDOCRINOL. 9:72-85(1995).
EMBL; U22015; G709961; --
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                                                                                                                                                                                                           VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; SIPHOVIRIDAE.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
LAZAREVIC V., DUESTERHOEFT A., SOLDO B., HILBERT H., MAUEL C.,
KARAMATA D.;
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Pred. No. 4.29e+00;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                              Length 178;
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01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
RETINOID X RECEPTOR INTERACTING PROTEIN 110 (FRAGMENT).
                                                                                                                                                                                                                                                                                  SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AF020713; G3025531; -. HYPOTHETICAL PROTEIN.
                                                                                                                  01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
HYPOTHETICAL 19-6 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 AA; 64852 MW; 28DA7406 CRC32;
                                                                                                                                                                                                                                                                                                                               178 AA; 19609 MW; CA7B8ED0 CRC32;
                                                                                        178 AA
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01-NOV-1996 (TREMBLREL. 01, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANNO
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                : |||: | |||:|| |
7 LQGRLQRLLQASGNHAAGIL 26
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1 MATRLQKALTEVGNHTTGNL 20
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Matches
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8; Conservative
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QGRLQRLLQASGNHAAGI 25
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                                                                                        PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                       RESULT 14
ID 064066
AC 064066;
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 3.36 Seconds 235.385 Million cell updates/sec Fri Aug 20 20:57:47 1999; Run on:

Tabular output not generated.

(1-28) from US08938548B.pep >US-08-938-548B-4 Title:

196 1 RSGPPGLQGRLQRLLQASGNHAAGILIM 28 Description: Perfect Score: Seguence:

PAM 150 Gap 15 Scoring table:

77977 segs, 28268293 residues Searched:

Post-processing:

0**%** Minimum Match Listing first

swiss-prot37 1:swissprot Database:

Mean 31.486; Variance 47.986; scale 0.656 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	5.54e-01	1.20e+00	2.55e+00	2.55e+00	2.55e+00	3.69e+00	3.69e+00	5.33e+00	5.33e+00	7.66e+00	7.66e+00	7.66e+00	7.66e+00	7.66e+00	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e+01
	Description	REGULATORY PROTEIN E2.	ADRENOLEUKODYSTROPHY P	NIFU PROTEIN.	RNA POLYMERASE PRINCIP	OLIGOMYCIN RESISTANCE	REGULATORY PROTEIN E2.	PROBABLE SULFATE ADENY	MITOCHONDRIAL PEPTIDE	ADENYLATE CYCLASE (EC	MITOCHONDRIAL 40S RIBO	ARGININOSUCCINATE SYNT	HYPOTHETICAL 63.2 KD P	PROBABLE DNA PACKAGING	HYPOTHETICAL 96.8 KD P	INTERLEUKIN-11 PRECURS	PULMONARY SURFACTANT-A	HYPOTHETICAL 28.7 KD P	ANNEXIN III (LIPOCORTI	PROTEIN UL88.	ECDYSONE RECEPTOR (ECD	STRUCTURAL POLYPROTEIN	PEROXISOME BIOSYNTHESI	THYROID RECEPTOR INTER
	ID	VE2_HPV63	ALD_MOUSE	NIFU_FRAAL	HRDB_STRCO	YOR1_YEAST	VE2_HPV09	NODQ_RHISB	RF1M_HUMAN	CYAA_SCHPO	RT04_YEAST	ASSY_SYNY3	YEAJ_ECOLI	VTER_EBV	YDBH_ECOLI	IL11_MOUSE	PSPA_HUMAN	YREC_SYNP2	ANX3_RAT	UL88_HCMVA	ECR_DROME	POLS_IPNVJ	PEX1_PICPA	TR12_HUMAN
	DB	-	-	Н	Н	Н	-	щ		1	Н	Н	ч	Н	-	٦	-	-	Н	Н	1	~	Н	7
	Match Length	398	736	79	442	1477	461	633	445	1692	394	400	556	069	879	199	248	256	324	429	878	972	1157	1992
% Query	Match	36.2	35.2	34.2	34.2	34.2	33.7	33.7		33.2	32.7	32.7	32.7	32.7	32.7	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1
	Score	71	69	29	67	29	99	99	65	65	64	64	64	64	64	63			63			63	63	63
Result	No.	П	7	m	4	വ	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

EXP X BY A BY A C. T.	OUTER MEMBRANE PROTEI FACTOR VIII INTRON 22 HYPOTHETICAL 78.9 KD ACONITATE HYDRATASE, HC-TOXIN SYNTHETASE (YOPM_YERPE F812_MOUSE YCBY_ECOLI ACON_BOVIN HTS1_COCCA	ннн н	367 380 702 780 5217	30.6 30.6 30.6 30.6	00000
PROTE SPHATE 8 KD P ROTEIN ON 22 9 KD P		AFSK_STRCO DCOP_MYCTU YP95_CAEEL YOPM_YERPE F812_MOUSE YCBY_ECOLI		799 274 302 367 380	31.1 30.6 30.6 30.6	
PRO	NEGATIVE FACTOR (F-PRO PULMONARY SURFACTANT-A MATING-TYPE LOCUS ALLE HYPOTHETICAL, 57 9 KD P	NEF_HVZNZ PSPA_PIG B7_USTMA VB77 VEAST		180 249 410 520		
Z E E	FATTY ACID SYNTHASE (E NEGATIVE RACINO)	FAS_HUMAN		2504	31.6	
NAD N		NIR_NEUCR KF1A_HUMAN		1176	31.6	
SIN	GLYCOPROTEIN B PRECURS STRUCTURAL POLYPROTEIN	VGLB_MCMVS POLS_IPNVN		928 972	31.6 31.6	
6	THERMOSTABLE CARBOXYPE SULFITE REDUCTASE (FER	SIR_SYNP7		511 624	31.6 31.6	
REGULA	01110111	CKEDE CKEC	4	374	31.6	

ALIGNMENTS

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"Two novel types of human papillomavirus, HPV 63 and HPV 65:

"Two novel types of human papillomavirus, HPV 63 and HPV 65:

"Omparisons of their clinical and histological features and DNA sequences to other HPV types.";

VIROLOGY 194:789-799(1993).

-! FUNCTION: EZ REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

-! FUNCTION: EZ REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE EZRE RESPONSE ELEMENT (5'-ACCNNNNNGGT-3') PRESENT IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPRINING OF EZRE'S POSITION WITH REGARDS TO PROWITER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSENBLY OF THE TRANSCRIPTION INITIATION COMPLEX. THE E1-EZ COMPLEX BINDS TO THE ORIGIN OF DNA HUMAN PAPILLOMAVIRUS TYPE 63. VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; PAPILLOMAVIRUS. SUBCELLULAR LOCATION: NUCLEAR. SUBUNIT: BINDS DNA AS A DIMER. 01-ocr'1994 (REL. 30, CREATED) 01-ocr'1994 (REL. 30, LAST SEQUENCE UPDATE) 15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE) REGULATORY PROTEIN E2. 398 AA PRT; STANDARD; SEQUENCE FROM N.A. MEDLINE; 93276568. REPLICATION. RESULT 1 ID VE2_HPV63 AC Q07850;

EMBL; X70828; G312096; -.
PFAM; PF00508; E2_N; 1.
PFAM; PF00511; E2_C; 1.
HSSP; P17383; 1DHM.
EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;

G FACTOR; DNA REPLICATION; REPRESSOR; NUCLEAR PROTEIN. 398 AA; 45450 MW; C9BBOCEO CRC32; TRANS-ACTING SEQUENCE 39

Length 398; 36.2%; Score 71; DB 1; I 55.6%; Pred. No. 5.54e-01; Query Match Best Local Similarity \sim

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NP_BIND
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CARBOHYD
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"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MALI locus reveals 15 complete open reading frames, including 2001, BGL2 and BIO2 genes and an ABC transporter gene.";
YEAST 13:251-259(1997).
-!- FUNCTION: REQUIRED FOR OLIGOMYCIN RESISTANCE.
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS). BELONGS TO THE MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMÝCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 96069397.

KATZMANN D.J., HALLSTROM T.C., VOET M., WYSOCK W., GOLIN J., VOLCRAERT G., MOYE-ROWIEX W.S.;

"Expression of an ATP-binding cassette transporter-encoding gene (YOR1) is required for oligomycin resistance in Saccharomyces cerevisiae.";
                                                                                                                         ö
                                                               Length 442;
                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOPROTEIN; TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (REL. 34, CREATED)
1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
0LIGOMYCIN RESISTANCE ATP-DEPENDENT PERMEASE YORI.
                                                            Score 67; DB 1; L
Pred. No. 2.55e+00;
   48413 MW; 4720321F CRC32;
                                                                                                                                                                                                                                                                                                                                                         PRT; 1477 AA.
                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOL. CELL. BIOL. 15:6875-6883(1995).
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PFAM; PF00064; ABC_membrane; 2.
HSSP: P13569; 1NBD.
ATP-BINDING; FRANSMEMBRANE; GLYC
                                                                                                                                                                            370 LQEQLHSVLDTLSEREAGVVSM 391
                                                                                                                                                                                                              | | :|: :|:: ::: ||:::| 7 LQGRLQRLLQASGNHAAGILTM 28
                                                      34.2%;
Similarity 31.8%;
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
MEDLINE; 97245295.
                                                                                        Best Local Similarity
      442 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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YOR1_YEAST
P53049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELIUS H., HOFMANN B.;

"Primer-directed sequencing of human papillomavirus types.";

CURR. TOP. MICROBIOL. IMMUNOL. 186:13-31(1994).

-!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNNGGT-3') PRESEN

IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER

ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION

WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN PAPILLOMAVIRUS TYPE 9.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; PAPILLOMAVIRUS.
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P17383; 1DHM.
EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
TRANS-ACTING FACTOR; DNA REPLICATION; REPRESSOR; NUCLEAR PROTEIN,
SPOHENCE 461 AA; 52141 MW; DA2B4125 CRC32;
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                                                                                                                                                                                                                                                                          Score 67; DB 1; Length 1477;
Pred. No. 2.55e+00;
6; Mismatches 6; Indels
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Pred. No. 3.69e+00;
6; Mismatches 10; Indels
                                                                                                                                                                                                                            79B302B8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
ID VE2_HPV09 STANDARD; PRT; 461 AA.
AC P36780;
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
ATP (POTENTIAL).
                    ATP (POTENT POTENT POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL.
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                                                                                            661: 661
759 759
179 799
1345 1345
1366 1366
1477 AA; 166727 M
                                                                                                                                                                                                                                                                                                                                                                                                        9 GRLQRLLQASGNHAAGILTM 28
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Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                          Query Match 34.2%;
Best Local Similarity 40.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                              8; Conservative
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628
1254
16
295
661
759
799
1345
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SEQUENCE FROM N.A.
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DAVIS S.C., TZAGOLOFF A., ELLIS S.R.,
"Characterization of a yeast mitochondrial ribosomal protein structurally related to the mammalian 68-kDa high affinity laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; FUNGI; ASCOMYCÒTA; HEMIASCOMYCETES; SACCHAROMYCETALES; SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEUCINE-REPEAT; CAMP SYNTHESIS; MAGNESIUM. 999 LEUCINE-RICH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYTIC.
20E7D7D8 CRC32;
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Pred. No. 5.33e+00;
3; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1993 (REL. 27, CREATED)
01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
MITOCHONDRIAL 40S RIBOSOMAL PROTEIN MR4.
MRP4 OR YHLO04W.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LER 3.
LER 4.
LER 6.
LER 6.
LER 7.
LER 7.
LER 9.
LER 10.
LER 11.
LER 11.
LER 11.
LER 12.
LER 14.
LER 14.
LER 15.
LER 16.
LER 16.
LER 17.
LER 17.
LER 17.
LER 17.
LER 18.
LER 19.
LER 20.
LER 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor."; J. BIOL. CHEM. 267:5508-5514(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00211; guanylate_cyc; 1.
PF00481; PP2C; 1.
PF00560; LRR; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190333 MW;
                                                                                                                                                                                                                                                                  EMBL, M26699; G173339; --
EMBL, M24942, G173379; --
EMBL, AL023859; E1298611; --
PIR, A33988; A33988.
PIR, A35398, A35359.
PFAM, PF00211; quanylate_cyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||||||:: :
4 PPGLQGRLQRLLQA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT;
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P32902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; P
LYASE;
DOMAIN
REPEAT
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REPEAT
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REPEAT
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REPEAT
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REPEAT
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REPEAT
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REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
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-!- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PYROPHOSPHATE + L-ARGININOSUCCINATE.
-!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINES, 97061201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HISOSOUI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.;
                                                                                                                                                                               ŗ.
                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
STRAIN=S288C / AB972;
MEDLINE; 94378003.
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
KUCRAA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUGER L.
WIRKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,
VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              RIBOSOME.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOMATION UPDATE)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                               SCIENCE 265:2077-2082(1994).
-!- FUNCTION: COMPONENT OF THE SMALL SUBUNIT OF MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 64; DB 1; L4
Pred. No. 7.66e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44151 MW; 5226C1B0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M82841; G171982; -.
EMBL; U10555; G500819; -.
PIR; S27429; S37429.
PIR; A42115; A42115.
SGD; L0001154; MRP4.
PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNECHOCYSTIS SP. (STRAIN PCC 6803).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00318; S2; 1.
RIBOSOMAL PROTEIN; MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.7%;
larity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 RAGQRGLQNRLAR 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSGPPGLQGRLQR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASSY_SYNY3 STP
P77973;
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARGG OR SLR0585.
                                                                                                                                                                                                                                                                                    VAUDIN M.;
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SIGNAL
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        STATES SOUND STATES
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                                                                                                                                                                                          AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOYO K., INDAA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAH H., KASHIHOTO K., KIM S., KIMMAS S., KITAGAWA M., KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y., NAKAMOTO H., MISHIO Y., OSHIMA T., SATIO N., SAMPEI G., SEKI Y., TAGAMI H., TAKENOTO K., WADA C., YAMANOTO Y., YANO M.; SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 97070356.

MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;

MOGRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;

"Modecular clohing and characterization of murine interleukin-11.";

EXP. HEMATOL. 24:1369-1376(1996).

-i- FUNCTION: THIS PROTEIN STIMULATES PLASMACYTOMA PROLIFERATION,
T-CELL-DEPENDENT DEVELOPMENT OF IMMUNOGLOBULIN-PRODUCING B
STRAIN=K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                BUNCH P.K., MAT-JAN F., LEE N.A., DEAYALA B.A., CLARK D.P.; SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                  MAU B., SHAO Y.;
"The complete genome sequence of Escherichia coli K-12.";
SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 1; Length 879;
Pred. No. 7.66e+00;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 36 I -> L (IN REF. 3).
879 AA; 96834 MW; 8BFD7CF3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
INTERLEUKIN-11 PRECURSOR (IL-11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNPUBLISHED OBSERVATIONS (MAR-1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000235; G1787646; -.
EMBL; D90776; G1742260; -.
EMBL; D90777; G1742264; -.
EMBL; U36928; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 GVDGRLQAILQAHENELGDFVLHM 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ::|||| :||| | : :| | 6 GLOGRLORLLOASGNHAAG-ILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watch 32.7%;
Local Similarity 45.8%;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-331 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECOGENE; EG13180; YDBH. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 15
IL11_MOUSE
P47873;
                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
CELLS AND SYNERGIZES WITH IL-3 IN SUPPORTING MURINE MEGARARYOCYTE COLONY FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63; DB 1; Loured. No. 1.10e+01;
                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
INTERLEUKIN-11.
; 1CB30772 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: Fri Aug 20 20:57:57 1999 Job time : 10 secs.
                                                                                                                                                                                                                                                                                                                           MGD; MGI:107613; IL11.
CYTOKINE; GROWTH FACTOR; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                              199 II
21522 MW;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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6 GLQGRLQRLLQ 16
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 20:57:08 1999; MasPar time 4.89 Seconds 229:521 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-4 101-28) from USO8938548B.pep 19 RSGPPGLQGRLQASGNHAAGILIM 28 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 30.618; Variance 52.462; scale 0.584 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.60e+00	3.24e+00	3.24e+00	4.58e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	9.07e+00	1.27e+01	1.27e+01	1.77e+01	1.77e+01	1.77e+01	1.77e+01	1.77e+01	1.77e+01	1.77e+01	1.77e+01
Description	hypothetical protein	hrpE protein - Pseudo	mALDP protein - mouse	hypothetical protein		c	transcription initiat	transcription initiat	transcription initiat	. probable ABC transpor	YOR1 protein - yeast	ı	E2 protein - human pa	calcium-binding prote	adenylate cyclase (EC	hypothetical protein	BGRF1 protein - human	ribosomal protein S2,	hypothetical protein	protein-tyrosine-phos	protein-tyrosine-phos	hypothetical protein	membrane protein ydbH
a	T02269	561858	S47044	E69913	T00987	S11712	S41307	JN0443	JN0445	T02644	564616	S23647	S36593	S26481	A33988	S51155	QQBE38	A42115	S76929	A46101	B46101	B64939	H64888
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% Query Match Length	511	439	736	178	145	442	510	525	528	1420	1477	2115	461	178	1692	263	325	394	400	3	548	256	879
% Query Match	36.2	35.2	35.2	34.7	34.2	34.2	34.2	34.2	34.2	34.2	٠	٠	•	٠	33.2	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.7
Score	71	69	69	68	49	49	29	49	49	49	29	67	99	65	65	64	64	64	64	64	64	64	64
Result No.	1	2	m	4	5	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

mitogen-activated pro 1.77e+01 pulmonary surfactant 2.46e+01 pulmonary surfactant 2.46e+01 pulmonary surfactant 2.46e+01 pulmonary surfactant 2.46e+01 hypothetical protein 2.46e+01 hypothetical protein 2.46e+01 hypothetical protein 2.46e+01 ecdysone receptor - f 2.46e+01 genome polyprotein - f 2.46e+01 probable cobN protein 2.46e+01 probable cobN protein 3.41e+01 allergen TBA-1 - Toxo 3.41e+01 deoxyuridine 5-tripho 3.41e+01 ranscription factor 3.41e+01 ranscription factor 3.41e+01 probable helicase pro 3.41e+01 glycoprotein B precur 3.41e+01 fatty-acid synthase (3.41e+01 fatty-acid synthase (3.41e+01	T.S.	te 3D8.6 - Arabidopsis thaliana s thaliana #common_name mouse-ear	evision 05-Mar-1999 #text_change	<pre>artz, J.R.; Kwan, A.; Toriumi, M.; Yu, ; Li, J.; Araujo, R.; Au, M.; Brendel, way, A.B.; Conway, A.R.; Dewar, K.; urtz, D.; Li, Y.; Palm, C.J.; Shinn, R.W.; Ecker, J.R.; Federspiel, N.A.;</pre>	ta Library, J omosome 1 BAC ated from GB/	NID:g3108025; PID:g3249066 11; 452/2; 477/3 weight 55547 #checksum 7824	71; DB 2; Length 511; . No. 1.60e+00; dismatches 7; Indels 0; Gaps 0;		te onas solanacearum s solanacearum evision 13-Mar-1997 #text_change 1, C.; Zischek, C.; Niqueux, E.; Arlat, cis, P.; German, S.; Castello, P.;
JE0363 151921 LNHUPS LNHUP1 03YCRQ 10RT3 S76765 S09852 A41055 GNXS1V A55152 E70940 B69081 S48361 B64899 JG2294 G71081 VGBEMC	ALIGNMENT	type complete protein T13D8 Arabidopsis t	sequence_revi	.; Schw Liu, S. E.; Con , C.; K	e EMBL liana y; tra bel VY	473 41 5ul	Score 7 Pred. N 4; Mi	AA 330 AA 23	Type complete - Pseudomonas - Pseudomonas so sequence_revis - F.; Gough, C.
011000000000000000000000000000000000000		tty P P	# S	ν.; Εκ.;	o the thal inary ##lab	4 6 #	2 5 5 6 8 9 7 6 9	STL	
1288 248 248 248 248 324 331 1157 11157 11157 11157 11157 11157 11157 1		T02269 #thypothetical #formal_name	ar-1999 -Mar-190	102269 214649 Yysotskaia, V.S.; Sc G. Oji, O.; Liu, V.; Buehler, E.; C Feng, J.; Kim, C.; Peng, J.; Kim, C.; Proj. J.; Kim, C.;	טשבע שופנה	EMB 8/3; 511	36.2%; ty 52.2%; servative	OSTPPGLOARAGRLVAAKSTLAA 	otei nam 1996 1996 1996 1996
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#molecule_type.
1.429,'0G',432-442 ##label SHI
##residues
##cross-references EMBL:X52983
##note
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transcription initiation factor sigma hrdB - Streptomyces
coelicolor
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#journal Gene (1991) 107:145-148
#title Sequence of hurbs, an essential gene encoding sigma-like transcription factor of Streptomyces coelicolor A3(2):
#cross-references MUID:92077425
#contents A3[2]
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03-May-1994 #sequence_revision 20-Feb-1995 #text_change
29-Jan-1999
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Tanaka, K.; Shiina, T.; Takahashi, H.
Science (1988) 242:1040-1042
Multiple principal sigma factor homologs in eubacteria:
identification of the "rpob box".
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submitted to the EMBL Data Library, April 1998
Arabidopsis thaliana chromosome II BAC 79722 genomic
                                                                                                                                                                                                               #length 145 #molecular-weight 15355 #checksum 3045
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submitted to the EMBL Data Library, May 1990
Multiple homolog genes for principal sigma subunit
Streptomyces coelicolor A3(2).
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                                      Length 145;
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##residues 1-442 ##label EMB
##cross-references EMBL:X52983; NID:g48744; PID:g48745
##experimental_source strain A3(2)
                                                                                                                                                                                                                                                  Score 67; DB 2; LA
Pred. No. 6.46e+00;
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#introns 17/1; 49/3; 78/2; 123/2
#note T9022.21
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                                                                                                                                                                                                                                                                                                                                           5 PGLQGRLQRLLQASGNHAAG 24
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Best Local Similarity 40.0%;
Matches 8; Conservative
                                    sequence.
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Marcos, A.T.; Diez, B.; Gutierrez, S.; Fernandez, F.J.; Velasco, J.; Martin, J.F. submitted to the EMBL Data Library, December 1993 organization and expression of the hrdB-sprC gene cluster of streptomyces griseus encoding a sigma factor protein and a serine protease. Role on growth and sporulation of
                                                                                                                                                                                                                                                                                                                                                                                                                         S41307 #type complete transcription initiation factor sigma - Streptomyces griseus
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#journal Gene (1992) 122:63-70
#title Four genes in Streptomyces aureofaciens containing a domain characterstic of principal sigma factors.
#cross-references MUID:93083996
                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Streptomyces griseus
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
29-Jan-1999
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#formal_name Streptomyces aureofaciens
30.Sep-1993 #sequence_revision 30-Sep-1993 #text_change
17.Mar-1999
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                                                   #domain transcription initiation factor sigma katF
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#length 510 #molecular-weight 55795 #checksum 1415
                                                                         homology #label KTF
#length 442 #molecular-weight 48413 #checksum 4794
DNA binding; sigma factor; transcription initiation
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##cross-references EMBL:X75952; NID:g440164; PID:g581664
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Pred. No. 6.46e+00;
11; Mismatches 4; Indels
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##molecule_type DNA
##residues 1-525 ##label KOR
##cross-references GB:M90411; NID:g153305; PID:g153306
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11; Mismatches 4;
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nes 7; Conservative
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Job time
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                                      KEYWORDS
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ENTRY
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                                                                                                                                                                                                                                                       ##residues 1-2115 ##label YAN
##cross-references EMBL:211583; NID:935118; PID:935119
##cross-references EMBL:211583; NID:935118; PID:935119
##note the authors translated the codon GAG for residue 781 as
61y, TTC for residue 1775 as Pro, and GGA for residue 2067 as GIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuan, R.S.; Fitzpatrick, D. submitted to the EMBL Data Library, September 1990 Structural analysis of mouse placental 57-KD Calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                          Yang, C.H.; Lambie, E.J.; Snyder, M.
J. Cell Biol. (1992) 116:1303-1317
NuMA: an unusually long coiled-coil related protein in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993 Primer-directed sequencing of human papillomavirus types. 336593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcium-binding protein, 57K - mouse
#formal_name Mus musculus #common_name house mouse
06.Jan-1995 #sequence_revision 06.Jan-1995 #text_change
10.sep-1997
     #formal_name Homo sapiens #common_name man
19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E2 protein - human papillomavirus type 9
#formal_name human papillomavirus type 9
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                      #molecular-weight 238273 #checksum 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-461 ##label DEL ##cross-references EMBL:X74464; NID:g397068; PID:g397073 ##cross-references EMBL:X74464; NID:g397068; PID:g397073 CLASSIFICATION #superfamily papillomavirus E2 protein DNA binding; early protein; transcription regulation sUMMARX #length 461 #molecular-weight 52141 #checksum 478
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                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Score 67; DB 2; Lv
Pred. No. 6.46e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                    mammalian nucleus.
*cross-references MUID:92176231
*accession $23647
NuMA protein - human
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                                                                                                                                                                                                                         preliminary
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Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.2%;
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 761 RAGRKGLEARLQQLGEA 777
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##residues 1-211
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#submission
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ORGANISM
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ORGANISM
               ORGANISM
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the authors translated the codon TGC for residue 626 as Ser, and GCC for residue 1243 as G1y #superfamily leucine-rich alpha -91ycoprotein repeat homology; yeast adenylate cyclase catalytic domain homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain yeast adenylate cyclase catalytic domain
                                                                             5316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:7989-7993
#title The adenylyl cyclase gene from Schizosaccharomyces
#cross-references MUID:90046723
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0
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0
                                                   calcium binding
#length 178 #molecular-weight 19960 #checksum
                                                                                                                                                                                                                                                                                                                                                                               A33988 #type complete
adenylate cyclase (EC 4.6.1.1) - fission yeast
(Schizosaccharomyces pombe)
#formal_name Schizosaccharomyces pombe
23.Mar-1990 #sequence_revision 23-Mar-1990 #tex
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Pred. No. 1.27e+01;
                                                                                                                        33.2%; Score 65; DB 2; Length 178; Similarity 30.8%; Pred. No. 1.27e+01; 8; Conservative. 9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young, D.; Riggs, M.; Field, J.; Vojtek, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-1692 ##label YOU ##cross-references GB:M26699; NID:g173338; PID:g173339
##residues 1-178 ##label TUA
##cross-references EMBL:X56603; NID:g53597; PID:g53598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references GB:M24942; NID:g173378; PID:g173379
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#length 1692 #molecular-weight 190332
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Similarity 57.1%;
8; Conservative
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##residues 1-1
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##residues 1-1
                                                                                                                                                    Local Similarity
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MPsrch_pp protein, - protein database search, using Smith-Waterman algorithm

Fri Aug 20 20:59:00 1999; MasPar time 1.72 Seconds 165.470 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-4 (1-28) from US08938548B.pep 196 1 RSGPPGLQGRLQRLLQASGNHAAGILIM 28 Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 15 Scoring table:

Searched:

106580 segs, 10152877 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Database:

Mean 20.494; Variance 80.948; scale 0.253 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	2.13e+01	2.59e+01	2.59e+01	2.59e+01	2.59e+01	2.59e + 01	3.14e+01	3.81e+01	3.81e+01	6.78e + 01	6.78e + 01	6.78e + 01	9.90e+01	9.90e+01	9.90e+01	9.90e+01	9.90e+01	9.90e+01	9.90e+01	9.90e+01	9.90e+01	9.90e+01	9.90e+01
	Description	Sequence 4, Applicatio	4	11,	12,	5, A	ý	'n	'n	Sequence 1, Applicatio	ģ	ý	10,	7	ω,	₹	Sequence 4, Applicatio	~	4	Sequence 2, Applicatio	14,	4, 2	Sequence 4, Applicatio	Sequence 14, Applicati
CTIVITION	ID	PCT-US95-1	US-08-363-	US-08-363-	US-08-363-	US-08-363-	US-08-804-	PCT-US91-0	US-08-858-	US-08-858-	PCT-US96-1	us-08-659-	ï	US-07-941-	US-08-792-	US-07-949-	US-08-814-	US-08-115-	US-08-017-	PCT-US93-0	US-07-745-	US-08-115-	US-07-941-	US-08-165-
	DB:	Μ	7	7	~	7	~1	m	~	N	ᠬ	~	Н	7	_		~	-	Η,	m	_	٦	-	7
	Length DB	716		442			184		381	381	176	176	2509	199	199	199	199	199	199	199	296	296	296	296
* Query	Match	34.7	34.2	34.2	34.2	34.2	34.2	33.7	33.2	33.2	31.6	31.6	31.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6
	Score	99	49	67	29	49	49	99	65	65	62	62	62	09	9	09	9	9	09	09	9	09	9	09
Result	Q	1	7	٣	4	5	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	

60 30.6 296 1 US-07-921- Sequence 14, Applicati 9 90e+01 60 30.6 296 3 PCT-US93-0 Sequence 4, Applicati 9 90e+01 60 30.6 296 3 PCT-US94-1 Sequence 14, Applicati 9 90e+01 60 30.6 528 2 US-08-363- Sequence 10, Applicati 9 90e+01 60 30.6 530 2 US-08-363- Sequence 10, Applicati 9 90e+01 60 30.6 530 2 US-08-363- Sequence 2, Applicati 9 90e+01 60 30.6 530 2 US-08-363- Sequence 2, Applicati 9 90e+01 60 30.6 530 2 US-08-363- Sequence 2, Applicati 9 90e+01 60 30.6 1271 2 US-08-363- Sequence 2, Applicati 9 90e+01 60 30.6 1271 2 US-08-444- Sequence 2, Applicati 9 90e+01 60 30.6 1271 2 US-08-444- Sequence 2, Applicati 9 90e+01 60 30.6 1271 2 US-08-444- Sequence 2, Applicati 9 90e+01 60 30.6 1271 2 US-08-444- Sequence 2, Applicati 1 199+02 59 30.1 829 1 US-08-446- Sequence 2, Applicati 1 1.99+02 10S-08-446- Sequence 2, Applicati 1 1.99+02 10S-08-406- Sequence 3, Applicati 1 1.99+02 10S-08-406- Sequence	ALIGNMENTS	1 :-US95-16311-4 STANDARD; PRT; 716 AA.	. xxx	quence 4, Application PC/TUS9516311	Sequence 4, Application PC/TUS9516311 GENERAL INFORMATION: APPLICANT: Moore, David APPLICANT: Moore, David APPLICANT: Seol, Wongi APPLICANT: Seol, Wongi APPLICANT: Choi, Hueng-sik TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS NUMBER OF SEQUENCES: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street, Suite 3100 STREET: 225 Franklin Street, Suite 3100 STREET: ADS COMPATY: USA COMPATY: USA COMPATY: USA COMPATY: Boston STREET: PROPPY disk COMPATY: BOSTON: PC-DOS/MS-DOS COMPATY: PREADABLE FORM: MEDIUM TYPE: Floppy disk COMPATY: PREADABLE FORM: MEDIUM TYPE: ROSPINS: PC-DOS/MS-DOS COMPATY: PREADABLE FORM: MEDIUM TYPE: ROSPINS: PC-TOS/MS-DOS COMPATY: PREADABLE FORM: MEDIUM TYPE: ROSPINS: PC-TOS/MS-DOS CURRENT REPARANTION DATA: APPLICATION NUMBER: PCT/US95/16311 RESISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 30,162 TELEPAX: 617/542-8906 TELEPAX: 2015-2070 TELEPAX: 176 amino acids TYPE: AMINO ACID
40000000000000044444444400000000000000		SULT PCT	XXXXXX		
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FITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION
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                                                                                                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/363,255
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS 32,430
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20002.22
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 813-5600
TELEFRAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08804227C
Patent NO. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Sotton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15.
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1841 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
NCE 445 AA; 48583 MW; 967304 CN;
                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08804227C
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                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 445 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                      ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
               NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 46285.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 34.2%;
Best Local Similarity 31.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: .....
STRANDEDNESS: S11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JT 6
US-08-804-227C-6
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                                                    APPLICANT: JACOBS, Jr., WILLIAM R.
APPLICANT: BLOOM, BARRY R.
APPLICANT: COLLINE, DESMOND M.
APPLICANT: CLISLE, GEOFFREY W.
APPLICANT: RAWAKAMI, RIKU P.
APPLICANT: KAWAKAMI, RIKU P.
TITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PRACELL Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 AA.
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Patent No. 578386
GENERAL INFORMATION:
APPLICANT: JACCOBS, Jr., WILLIAM R. APPLICANT: BLOOM, BARRY R. APPLICANT: COLLINS, DESMOND M. APPLICANT: GELISLE, GEOFFREY W. APPLICANT: PASCOPELLA, LISA APPLICANT: RAWAKAMI, RIKU P. TITLE OF INVENTION: MYCOBACTERIA VIR
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,255
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
ICE 445 AA; 48583 MW; 967304 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
         Sequence 12, Application US/08363255
Patent No. 5783386
GENERAL INFORMATION:
                                                                                                                                                                              NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2523
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08363255
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 LQEQLHSVLDTLSEREAGVVSM 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | :|: :|: ::: | |:::| 7 LQGRLQRLLQASGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity 31.8%;
Matches 7; Conservative
                                                                                                                                                                                                                STREET: 755 CITY: Palo Alto
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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LOCATION: 1.176
OTHER INFORMATION: /note= "rev protein encoded by HIV-2KR"
NCE 176 AA; 19639 MW; 145168 CN;
                                                                                                                                                                     Sequence 6, Application PC/TUS9611445
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California ATILLE OF INVENTION: Isolation of Novel HIV-2 Proviruses NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCI/US96/11445
FILING DATE:
CLASSIFICATION:
ATTORNEY/ACTO:
ATTORNEY/ACTO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62; DB 3; Length 176;
Pred. No. 6.78e+01;
5; Mismatches 9; Indels
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COMPUTER: The PPC T
  176 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-399C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEPHONE: (213) 977-1003
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Patent No. 5883081
GENERAL INFORMATION:
APPLICANT: Kraus, Guenter
APPLICANT: Wong-Staal, Flossie
APPLICANT: Talbott, Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08659251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS:
  STANDARD;
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Best Local Similarity 40.0%;
Matches, 10; Conservative
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PCT-US96-11445-6
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US-08-659-251-6
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                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08858052
Patent No. 5849498
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HYDROLASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 3.81e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,052
                                                                                                                                                     381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0294 US
TELECOMMINICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 AA; 42808 MW; 739653 CN;
                                                                                                                                                     PRT;
                296 KMSPTSLKITLRQLMEGSSKTLQEVLTM 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 KMSPTSLKITLRQLMEGSSKTLQEVLTM 323
                                             Sequence 1, Application US/08858052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ILENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.2%;
Best Local Similarity 28.6%;
Matches 8; Conservative
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CLONE: 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
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PRT;
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JENCE 199 AA; 21429 MW; 188641 CN;
                                                    TION: -21..0
199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: Fri Aug 20 20:59:08 1999
                                                                                                                                                                                                                                        Sequence 4, Application US/07949516A
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.6%;
Best Local Similarity 70.0%;
                                                                               Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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               Protein
                       1..178
                                         NAME/KEY: Region
                                                                                                                      129 LQARLDRLLR 138
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                                                                                                                                        7 LOGRIQRILQ 16
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             NAME/KEY:
LOCATION:
FEATURE:
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US-07-949-516A-4
                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Job time : 8 secs
    FEATURE:
                                                             SEQUENCE
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Pred. No. 9.90e+01;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08792019B
Patent No. 574172
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: CHANG, MING-SHI
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/07/941,372
FILING DATE: 19920902
                                                                                                                                                                                                                                                                                                                   199 AA.
                                                                           NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDUSI
TELECOMMUNICATION INFORMATION:
TELEFRON: (215) 540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08792019B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INC.

NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31,602

REFERENCE/DOCKET NUMBER: A--

RFORMATION FOR SEQ ID NO: 8:
                                               FILING DATE: 19920902
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                  Query Match 30.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                         LT 14
US-08-792-019B-8
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/949,516A
FILING DATE: 19-NOV-1992
CLASSIFICATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: 31,544
REFERENCE/DOCKET NUMBER: 5174BPCT
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEBOTH: 199 annino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; DB 1; Length 199;
Pred. No. 9.90e+01;
3; Mismatches 0; Indels
Score 60; DB 1; Length 199;
Pred. No. 9.90e+01;
                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/07949516A
Patent No. 5700664
GENERAL INFORMATION:
APPLICANT: Yang, Yu-Chung
APPLICANT: Bennett, Frances
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                             199 AA
                                           3; Mismatches
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

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Tabular output not generated.

>US-08-938-548B-4 (1-28) from US08938548B.pep Description: Perfect Score: Title:

1 RSGPPGLOGRLORLLOASGNHAAGILTM 28 Sequence:

Scoring table:

PAM 150 Gap 15

Searched:

170751 seqs, 21266608 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part14 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Variance 88.246; scale 0.250 Mean 22.064; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	7.83e-11	3.06e-10	3.06e-10	3.06e-10	3.06e-10	6.30e+01	7.60e+01	7.60e+01	7.60e+01	7.60e+01	7.60e+01	7.60e+01	9.16e+01	1.10e+02	1.60e+02	1.60e+02
Description	Human HFGAN72 recepto	Mouse HFGAN72 recepto	Mouse hypocretin 35.	Rat hypocretin 35.	Rat HFGAN72 receptor	Retinoid X receptor i	S. cerevisiae scaur2R	Saccharomyces cerevis	Tylactone synthase OR	LexA/NuMA fusion prot	GAL4/HA/NuMA fusion p	Streptomyces venezuel	"p33" N-terminal (2).	Human 3-hydroxyisobut	New polypeptide based	Vector PSP 35K-1A-10
ID	W61381	W61383	W50158	W50157	W61382	R99737	R67691	W10424	W22605	W21732	W21731	W19629	R20235	W81135	R00579	R05091
DB	33	33	30	30	33	18	13	22	56	23	23	23	4	38	Н	~
% Duery Match Length	131	123	130	130	130	716	1477	1477	1841	2192	2272	4630	10	381	32	248
% Query Match	100.0	6.96	6.96	6.96	6.96	34.7	34.2	34.2	34.2	34.2	34.2	34.2	33.7	33.2	32.1	32.1
Score	196	190	190	190	190	68	67	67	67	67	49	49	99	65	63	63
Result No.		7	m	4	ស	9	7	∞	σ	10	11	12	13	14	15	16

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Human alveolar surfac Plasmid pASPcq-SV(10) Human 32K ASP encoded Sequence deduced from 35kd nulmonary surfac	uman 32k ASP enco equence deduced f 5kd pulmonary sur enomic sequence o	nce of hu id pASPc- ic sequer 32K alve	Human 32K ASP encoded Ecdysone receptor lig Drosophila ecdysone r Modified ecdysone rec Modified ecdysone rec	ha protein. receptor. ecdysone re ovirus-encod	Protein (OA-519) cros Human interleukin 11 A human mutant alanin Virulence-associated Human KM-102-derived Platenolide synthase
R06331 P60442 R04215 P82980	0421 8069 7066 6066	25645	421 913 365 365	30508	W32881 W02202 W46904 R76480 W83404
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ALIGNMENTS

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PR 26-SEP-1995; US-939093.

PR 26-SEP-1996; US-939093.

PR 17-DEC-1996; US-82019.

PR 17-DEC-1996; US-82019.

PR 17-DEC-1996; US-82019.

PR 02-JUL-1997; US-82019.

PA (SMIK ) SMITHKLINE BEECHAM FOLC.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PA (SMIK ) SMITH SECHAM PLC.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PA (SMIK ) SMIKHLINE BEECHAM PLC.

PA (SMIKH ) SMIK
                                                                                             Human HFGAN72 receptor protein.

HFGAN72 receptor; eating disoclars; renal disease; heart failure; sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention; osteoporosis; angina pectoris; myocardial infarction; psychotic disorder; neurological disorder.
                                                                                                                                                                                                                                                                                                                                  34..66
/note= "Ligand 72A"
70..97
/note= "Ligand 72B"
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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T 1
W61381 standard; Protein; 131
                                                                                    (first entry)
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                                                                                                                                                                                                                                                                         Homo sapiens
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                                                     W61381;
02-OCT-1998
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Matches
                               RESULT
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Claim 5: Fig 4: 35pp: English.

Claim 6: Fig 4: 5pp: English.

Claim 6: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat HFGAN72 receptor protein.
HFGAN72 receptor; eating disorders; renal disease; heart failure; sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention; osteoporosis; angina pectoris; myocardial infarction; psychotic disorder; neurological disorder.
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antagonists, in therapy, to detect Ab and to isolate cognate receptors. Oligonucleotides based on H35 cDNA can be used to detect the hypocretin gene or its RNA transcript, and as antisense agents for inhibiting gene expression. H35 cDNA can also be used for recombinant protein production. The Ab can be used to detect or quantify hypocretin proteins and as a therapeutic inhibitor.
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                              DB 30; Length 130;
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                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                         Score 190; DB 30; Pred. No. 3.06e-10;
                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                       69 rpgppglqgrlqrllqangnhaagiltm 96
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/note= "Ligand 72A"
69..96
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92.98;
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les 26; Conservative
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17-DEC-1996; US-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
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                                                                                                                                         130 AA;
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17-DEC-1997;
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W61382
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                                                                                                                                                                                                                                                                                                Refinoid X receptor (RXR) interacting protein (RIP) - useful to medulate or mediate RXR function, anti-RIP antibodies can be used to determine RIP subcellular distribution patterns

Claim 2: Page 48-50; 90pp; English.

Mouse retinoid X receptor (RXR) interacting protein RIP110 (R99737) is a candidate transcriptional co-activator. It was identified using an in vivo interaction trap system for the isolation of proteins that physically interact with RXRs, esp. with the ligand binding domain of human RXR alpha. Recombinant RIP110 can be obtd. using a cDNA clone (731930) obtd. from a mouse liver library. RIPS (see also R99735-35 and R99738-39) can be used to modulate or mediate RXR function, and may be used therapeutically or to raise antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 77-84; 110pp; English.
Saccharomyces cerevisiae DKD5D, which is sensitive to aureobasidin, was mutagenized with EMS and genomic libraries of 2 resistant strains were prepared. Resistant gene scaurlR (Q75954) was isolated from 1 library, and resistant gene scaurlR (Q75956) from the other. A DNA fragment of scaurl was used as a probe to isolate a sensitive gene, scaurlS (Q75955), from the sensitive strain. A TB52A mutation leading to a F158Y conversion gave rise to the resistance of scaurlR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New genes regulating aureobasidin sensitivity - used to develop prods. for the diagnosis and treatment of diseases such as
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                                                              Retinoid X receptor interacting protein RIP110.
Retinoid X receptor interacting protein; RXR; RIP; RIP110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 716;
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Pred. No. 6.30e+01;
6; Mismatches 4;
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S. cerevisiae scaur2R gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R67691 standard; Protein; 1477 AA
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  standard; Protein; 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.2%;
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Best Local Similarity 44.4%;
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08-DEC-1995; U16311.
13-JAN-1995; US-372652.
(GEHO ) GEN HOSPITAL CORP.
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                                          27-SEP-1996 (first
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WPI; 95-023286/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1477 AA;
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                                                                                                                                                                                                                                                                 WPI; 96-342241/34.
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                                                                                                           Mus sp.
WO9621677-A1.
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Gaps

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69 rpgppglqgrlqrllqangnhaagiltm 96

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WPI; 97-341701/31.
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                                                   industrial use
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The sequences given in W21731-32 represent fusion proteins which contain NuMA (nuclear mitticis apparatus). The fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30).

W21729-30). Compounds which interfere with the interaction of NuMA with a known NIP are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NUMA or NIP, it can be treated by administration of the appropriate functional protein.
                                                                                               01-OCT-1997 (first entry)
02AL4/HA/NuMA fusion protein.
08L4/HA/NuMA fusion protein.
NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NuMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth.
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                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding nuclear mitotic appts. interacting proteins - useful for modulating cell division and proliferation and in diagnosis
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Streptomyces venezuelae polyketide synthase.
Polyketide synthase, polyhydroxyalkanoate monomer synthase;
polyhydroxybutyrate; biodegradable polymer; vep gene;
metabolic engineering.
Streptomyces venezuelae.
W09722711-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                    /label= Residues_18-2116_of_NuMA 365..1864
                                                                                                                                                                                             /label= GAL4_DNA_binding_domain
148..174
/label= Hemaglutinin_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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                                                                                                                                                                        Location/Qualifiers
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W19629 standard; Protein; 4630 AA.
W19629;
                                                                      W21731 standard; Protein; 2272 AA. W21731;
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18-DEC-1995; UZ-008847.
MINU) UNIV MINNESORA.
Sherman DH, Williams MD, Xue Y;
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Best Local Similarity 52.9%;
Matches 9; Conservative
838 ragrkglearlqqlgea 854
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WPI; 97-077270/07.
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1 RSGPPGLQGRLQRLLQA 17
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07-JUN-1995, US-478408.
(UYXA ) UNIV YALE.
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                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                    WO9640917-A1
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PF 116
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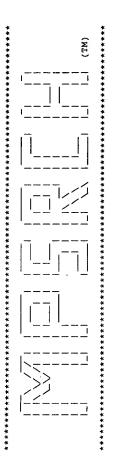
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Claim 55; Fig 23; 91pp; English.

Claim 55; Fig 23; 91pp; English.

Claim 55; Fig 23; 91pp; English.

Claim 55; Pig 23; 91pp; English.

Claim 56; Pig 23; 91pp; Pig 25; Pig 26; 
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Claim 1; Page 60; 75pp; English.
A protein, designated p33, is found on the surface of several types of lymphocyte cells, including OKT3-stimulated primary T-cells, antigen-specific IL-2 dependent CTL clones, and a PMA-stimulated human T-cell hybridoma, IL-23.D7. It forms a novel complex with lymphotoxin (LT). The N-terminal of the p33 protein contains the sequence represented in R20234 or R20235. The sequence at the 6th cycle appeared to be a mixt. of both G and L indicating possible polymorphism. The p33 protein may have one of these sequences or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Expression cassettes for production of polyhydroxyalkanoate(s) provide wide range of biodegradable polymers for medical or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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Pred. No. 7.60e+01;
....matches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New membrane associated protein, p33 - forms complex with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 4; Length 10;
Pred. No. 9.16e+01;
1; Mismatches 0; Indels
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"p33" N-terminal (2).
MAP; lymphocyte; IL-2; CTL; polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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W81135 standard; Protein; 381 AA.
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R20235 standard; Protein; 10
R20235;
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Best Local Similarity 33.3%;
Matches 8; Conservative
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(REGC ) UNIV OF CALIFORNIA.
Browning J, Ware CF;
WPI; 92-041521/05.
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Similarity 88.9%;
8; Conservative
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27-JUN-1991; U04588.
27-JUN-1990; US-544862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4630 AA;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:00:11 1999; MasPar time 7.71 Seconds 358.518 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-938-548B-6 (1-130) from USO8938548B.pep 954 Description: Perfect Score:

1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATALAPRGGSRV 130 Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseg35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part19 20:part16 16:part16 17:part11 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38 Database:

Mean 30.024; Variance 131.695; scale 0.228 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description Pred. No.		hypocretin 35. 5.23e-79	HFGAN72 receptor 5.23e-79	hypocretin 35. 6.08e-73	HFGAN72 recepto	HFGAN72 recepto 1.76e-62	cell line-deriv	cell line-deriv 4.	A GDNFR-alpha-related 4.63e-01	GDNF alpha-3 re 4.		Ret ligand RetL 4.	Human fibulin type 1 9.01e+00		in B. 9.01e+00	Human fibulin type 1 9.01e+00	5
SOMETHING			ID		W50157 Rat hy	W61382 Rat HE	W50158 Mouse	W61383 Mouse	W61381 Human	W84185 Glial	W84186 Glial	W84180 A GDNE	W65116 Human	W65117 Human	W37463 Human		R11148 Fibulin A.	R11149 Fibulin B.		R11150 Fibulin C.
			gth DB		130 30	130 33	130 30	123 33	131 33	378 39	400 39	400 39	400 32	400 32	400 28	556 28	566 2	601 2	601 28	683 2
	æ	Query	Match Length DB	1 1 1 1 1 1 1		100.0	93.4	89.4	82.0	11.8		11.8		11.8						
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Gaps

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Score 954; DB 30; Length 130; Pred. No. 5.23e-79; 0; Mismatches 0; Indels

Query Match 100.0%; Best Local Similarity 100.0%; Matches 130; Conservative

Human fibulin type 1 Human fibulin type 1 Human fibulin type 1 Human lecithin choles 2.10e+01 Human N-proteinase (7 Human N-proteinase (7 Human Secreted protes (1 Truncated Platelet de 2,93e+01 Human PDGP-B precurso 2,93e+01 Platelet derived Grow 2,93e+01 Pogr Bc-sis. 2,93e+01 Pogr Bc-sis. 2,93e+01 Pogr Bc-sis. 2,93e+01 Pogr Bc-sis. 3,94e+01 Human 4.1BB-L polypep 3,46e+01 Human 4.1BB-L polypep 3,46e+01 Tryptophan aporepress 3,66e+01 Tryptophan aporepress 4,08e+01 Sequence encoded by p 4,08e+01 Recombinant platelet 4,08e+01 Human aspartic protea 4,08e+01	HESULT 1 The Wasser of the Management of the Ma
W27600 W27601 W20160 W720189 W72028 W47029 W47029 W470028 W470028 W470005 R50005 R50009 R50009 R63469 R21708 R21708 R21708 R21708 R21708 R21708 R21708 R21708 R21708 R21708 R21708 R21708	W50157 standard; Protein; 130 AA. W50157; W501
22 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	The policy of th
0883 1774 1774 1774 1774 1774 1774 1774 177	; Protein; 35. 435; function; ulatory ho ulatory ho duff TS, S 3657. 1867. 1867. 1867. 1867. 1868. 1869. 18
	rd; in 35; in 35; i
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$\begin{smallmatrix} 2&2&2&2&2&2&2&2&2&2&2&2&2&2&2&2&2&2&2&$	W50157 stand W50157, stand W50157, stand W50157, work by borner Rat hypocret Rat hypocret Ratts hypocret Rattus rattu W0805352-A1 W0805352-A1 W090605352-A1 W18 W19 98-1453 N-PSDB; V188 Nucleic acid diagnosis and
11112222222222222222222222222222222222	WAT THE BUNE RELEACE RESERVE OF THE REPRESENTATION OF THE PROPERTY OF THE PROP
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Claim 2, Fig 2; 35pp; English.

The HFGAN72 receptor protein contains two ligands whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bulnina, cachexia, chronic renal failure, remaind lasease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating ancrevisa, bulinia and cachexia. The HFGAN72 receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, Parkinson's disease, both acute and congestive heart failure, hypotension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign pectoris, myocardial infarction, ulcers, asthma, allergies, benign concestic hypertrophy, chronic renal failure, renal disease, impaired glucose tolerance, sexual dysfunction and psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glial cell line-derived neurotrophic factor receptor gamma 1.

Glial cell line-derived neurotrophic factor receptor gamma 1;

GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;

neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gammal;

Parkinson's disease; schizophrenia; insomnia; tardive dyskenisia;

hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;

renal disorder; kidney failure; gut dysfunction; regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 agiltlgkrrsgppglggrlgrllgasgnhaagiltmgrragaepaprpclgrrcsapaa 120
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27-UN-1997; US-884638.
20-MAY-1997; US-88004638.
4HUMA-) HUMAN GENOME SCI INC.
Gentz RL, HSU T, Ni J, Ruben SM, Young P;
WPI: 99-0701507/06.
N-PSDB; V99333.
New isolated glial cell derived neurotrophic factor receptors - used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 33; Length 131;
                                          N-PSDB; V28138.
HFGAN72 receptor ligands - and corresponding DNA, agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 782; DB 33; Length 13
Pred. No. 1.76e-62;
10; Mismatches 7; Indels
DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease or Gilles dela Tourett's syndrome.
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32..360
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W84185 standard; Protein; 378 AA.
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Best Local Similarity 85.2%;
Matches 109; Conservative
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                         98-324672/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HFGAN72 receptor; eating disorders; renal disease; heart failure;
sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or Gilles dela Tourett's syndrome.
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                                                                                                                                                                                                                                                                  HFGAN72 receptor ligands - and corresponding DNA, agonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. (SMIX ) SMITHKLINE BEECHAM PLC. Bergsam DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M; WPI; 98-324672/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 853; DB 33;
Pred. No. 2.73e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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34..66
/note= "Ligand 72A"
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17-DEC-1996; US-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 5
W61381 standard; Protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human HFGAN72 receptor protein.
                                                                                                                                                                                                                                                                                      antibodies, antagonists, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 89.4%;
Best Local Similarity 95.1%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W61381;
02-OCT-1998 (first entry)
                                                                 26-SEP-1997; US-939093
17-DEC-1996; US-033604
                                                                                                              19-MAR-1997; US-820519
02-JUL-1997; US-887382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70..97
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26-SEP-1997; US-9390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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2; Gaps

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Therve cells

Claim 2: Page 85-86; 113pp; English.

This amino acid sequence comprises human Ret ligand (RetL) RetL3, Caduced from acid sequence comprises human RetL1, human RetL2 and and spinal cord libraries. Rat and human RetL1, human RetL2 and mouse RetL3 sequences (see W37457-62) are also claimed. Human RetL1 is 34.3% identical to human RetL1, 34.9% identical to human RetL1, and 76.8% identical to human RetL1, 34.9% identical to human RetL1 is 34.3% identical to human RetL1, and 76.8% identical to human RetL1, is 43.3% identical to human RetL1, and 76.8% identical to human RetL1, is 43.3% identical to human RetL1 is 34.3% identical to human RetL1 is 34.3% identical to human RetL1 interacts with Ret receptor protein, triggering Ret dimerisation and/or autophosphorylation of the Ret tyrosine kinase domain.

Vectors containing retL3 DNA and prokaryotic or eukaryotic host or land and proteins with a toxin, imageable compound or radionuclide.

Vectors containing retL3 DNA and prokaryotic or eukaryotic host calls transformed or transfected with these vectors are claimed, as well as a method for production of RetL3, its soluble variants and fusion proteins with a toxin, imageable compound or radionuclide.

RetL3, optionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue, particularly kidney or neural tissue. Typical applications are in renal failure, nephritis, kidney transplants, toxic or hypoxic injury, meurodegeneration, motor neurone disease, mutitly associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury, developmental discorders such as Down's syndrome system (Lyme disease, muscular dystrophy and myasthenia gravis).

Fision proteins are used to deliver toxins etc. to Ret-expressing
This sequence represents a novel glial cell line-derived neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases (including the muscular dystrophies) and nerve and sequence 400 AA;

    vectors, transformed cells and antibodies, used for promoting cell
growth and improving survival of injured cells, especially renal or

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding ret receptor ligands and related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Ret ligand Retu3.

Ret ligand; Retu3.

Ret ligand; Retu3. receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; meningitis; myelopathy; Creutzfeldf-Jakob disease; candal nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
                                                                                                                                                                                                                                                      Score 113; DB 32; Length 400;
Pred. No. 4.63e-01;
9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                        9 plppvvlm11111ppsplplaa-gdplptesrlmn-sc 44
                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    9 PWAAVILLILLILPPALLSLGVDAQPLPDCCRQKTCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Sanicola-Nadel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myasthenia gravis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JT 11
W37463 standard; Protein; 400 AA
                                                                                                                                                                                                                                                            Query Match 11.8%;
Best Local Similarity 47.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                     18; Conservative
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07.MAY-1997; U07726.
10.APR-1997; US-017427.
08.MAY-1996; US-017427.
07.JUN-1996; US-018930.
16.JUL-1996; US-021859.
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N-PSDB; V00251.
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Human GDNF alpha-3 receptor protein #2.
Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;
amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
muscular dystrophy; diagnostic.
                                                     28-SEP-1998 (first entry)

Human GDNF alpha-3 receptor protein #1.

Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF; treatment; neurodegenerative disease; Parkinson's Disease; ALS; SNA; amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma; Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used to treat neuro degenerative diseases, muscular diseases and nerve and muscle trauma and in diagnostic assays

Claim 4; Fig 2; 22pp; English.

This sequence represents a novel glial cell line-derived neurotrophic factor alpha-3; receptor (GDNF alpha-3). This protein can be used to treat e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases (including the muscular dystrophies) and nerve and muscle trauma and in diagnostic assays for such conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 4.63e-01;
9; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 plppvvlmlllllppsplplaa-gdplptesrlmn-sc 44
                                                                                                                                                                                                                                                                                                                                                                  /note= "Partial sequence"
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/label= GDNF alpha-3
                                                                                                                                                                                                                                                                                                                                           /label= GDNF alpha-3
                                                                                                                                                                                                                                                                                   Location/Qualifiers
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W65117 standard; Protein; 400'AA.
        W65116 standard; Protein; 400 AA
                                                                                                                                                                                                                                muscular dystrophy; diagnostic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 11.8%;
Local Similarity 47.4%;
les 18; Conservative
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20-NOV-1997; 309375.
09-MAY-1997; GB-009463.
27-NOV-1996; GB-024677.
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20-NOV-1997; 309375.
09-MAY-1997; GB-009463.
27-NOV-1996; GB-024677.
                                                                                                                                                                                                                                                                                                            .400
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N-PSDB; V35364.
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Bennett LG;
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                                                                                                                                                                                                                                                               Gaps
single residue. Embodied within repeats 5, 6, 7 and 8 is the consensus sequence for Asp and Asn hydroxylation. The 7th repeat contains the consensus O-gycosylation sequence. CXCXPC.
Immediately following each repeat is a pentapeptide with the consensus sequence XD(I/V)(D/N)E. Fibulin binds to the cytoplasmic domain of the betal subunit of integrin adhesion receptors in a cation dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, with the protein have important diagnostic and therapeutic uses. See also RI1147, RI1149 and RI1150.
                                                                                                                                                                                                                         Score 96; DB 2; Length 566; Pred. No. 9.01e+00; 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibulin B.
Beta-1 integrin; adhesion; receptor; fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= N-linked glycosylation
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220..260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..29
/label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36..69
/label= repeat unit 1
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/label= repeat unit 2
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/label= type II motif
180..214
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261..265
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307..311
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/label= repeat unit 4
355..359
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398..402
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440..444
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/label= type I motif
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/label= fibulin B
                                                                                                                                                                                                                                                                                                                                                                                             R11149 standard; Protein; 601 AA.
                                                                                                                                                                                                                         Query Match 10.1%;
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          R11149;
21-MAY-1991 (first entry)
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                                                                                                                                                                                          566 AA;
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                                                                                                                                                                                          Sequence
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Sclaim 10; Fig 4; 56pp; English.

Claim 10; Fig 4; 56pp; English.

The fibulin A, B and C forms are identical from their N-terminals to a divergence point at posn. 566 ( terminal codon in fibulin A)

and 683 residues resp.

All three forms are rich in cysteine (11 %) and 683 residues resp. All three forms are rich in cysteine (11 %)

and analysis wrt no. and spacing of the Cys residues revealed two types of repeat moftif (I and II). The type I motif, CC(X)12c-

C(X)9-10C(X)6CC is repeated twice, separated by an imperfect form of the repeat lacking two Cys residues. The same motif is found in complement components C3a, C4 and C5a; the inverse is found in complement components C3a. The same motif is found in complement components C3a. The same motif is found in complement components C3a. The same motif is found in complement cursor is a 6-Cys pattern repeated nine times, although the type II motif, related to repeats found in epidermal growth the city precursor is a 6-Cys pattern repeated nine times, although the mosensus sequence for Asp and Asn hydroxylation. The 7th repeat consensus sequence for Asp and Asn hydroxylation. The 7th repeat consensus sequence EX(I/V)(D/N)E. Fibulin binds to the cyto.

Immediately following each repeat is a pentapeptide with the consensus of the betal subunit of integrin adhesion receptors in a cation-dependent, EDTA-reversible manner. It can receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibromethic, collagen, laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses.

Sequence for an important diagnostic and therapeutic uses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Human fibulin type 1 isoform (variant B).

Human fibulin protein; met-OB protein; hypertension; obesity; isoform; type II diabetes; fibrogenesis.

Homo sapiens.

W09738014-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 2; Leny L..
5. 9.01e+00;
1. 2. 8; Indels
                                                                                                                                                                                                                               530..535
/label= consensus pentapeptide
/label= consensus pentapeptide
                                                                                                                          label consensus pentapeptide
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Pred. No.
                                                                  'label= repeat unit 7
                                                                                                                                                                                                       repeat unit 8
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W27599 standard; Protein; 601 AA.
W27599;
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Best Local Similarity 57.1%;
Matches 16; Conservative
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WPI; 91-087250/12.
N-PSDB; Q11009.
                                  ..479
                                                                                                 ..484
                                                                                                                                                                485..529
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18-AUG-1989; US-395773.
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03-APR-1997; U06280.
04-APR-1996; US-627636.
(AMGE-) AMGEN INC.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:02:20 1999; MasPar time 11.91 Seconds 595.879 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-6 (1-130) from USO8938548B.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130

Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 40.229; Variance 88.216; scale 0.456

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No.
954	100.0	130	: :	055232	PREPRO-OREXIN.	1.31e-153
894	93.7	130	11	055241	HYPOCRETIN (PREPRO-ORE	3.25e-142
782	82.0	131	4	043612	PREPRO-OREXIN.	4.87e-121
756	79.2	131	9	077668	PREPRO-OREXIN PRECURSO	3.82e-116
113	11.8	400	4	609090	GDNF FAMILY RECEPTOR A	5.76e-03
106	11.1	619	10	023352	HYPOTHETICAL 74.6 KD P	4.77e-02
86	10.3	574	1	035298	ACYLOXYACYL HYDROLASE.	4.90e-01
86	10.3	641	11	008463	FRIZZLED PROTEIN HOMOL	4.90e-01
96	10.1	272	Ŋ	077465	LARGE RIBOSOMAL PROTEI	8.63e-01
96	10.1	626	1	070421	FRIZZLED-1.	8.63e-01
96	10.1	920	7	087342	BETA-(1-3)-GLUCOSYL TR	8.63e-01
92	9.6	106	10	041051	PROLINE- AND LEUCINE-R	2.62e+00
91	9.5	440	11	035849	LECITHIN: CHOLESTEROL A	3.45e+00
90	9.4	833	4	099523	SORTILIN PRECURSOR.	4.53e+00
83	9.3	144	4	075779	COLIA1 AND PDGFB FUSIO	5.93e+00
8	9.3	154	4	015186	COLIA1 AND PDGFB FUSIO	5.93e+00
8	9.3	175	4	060895	MRNA ENCODING RAMP2 PR	5.93e+00
8	9.3	185	4	015354	C-SIS PROTO-ONCOGENE (5.93e+00
8	9.3	331	13	091640	LEUCINE ZIPPER WITH BA	5.93e+00
83	9.3	1321	4	075129	KIAA0634 PROTEIN (FRAG	5.93e+00

7.74e+00 7.74e+00 1.01e+01	1.01e+01	1.01e+01 1.01e+01 1.31e+01	1.31e+01		1.31e+01	1.31e+01	1.31e+01 1.71e+01	1.71e+01	1.71e+01 1.71e+01	1.71e+01	1.71e+01	2.21e+01	2.21e+01	2.21e+01
HYPOTHETICAL 23.1 KD P TIGHT JUNCTION PROTEIN V-SIS TRANSFORMING PRO	BETA-LAC BIOSYNTE	DNA BINDING PROTEIN EI SIMILARITY TO MOUSE SM PITATIVE GPI-ANCHORED	LEUCINE-RICH RECEPTOR- NB-2.	(STRAIN OREGON) P125 (SINITESE.	N.	POLYKETIDE SYNTHASE MO NHOA.	Ĕ,	PUTATIVE G PROTEIN-COU PUTATIVE ENDOTHELIN RE	G PROTEIN COUPLED RECE	RNA-DEPENDENT RNA POLY	ANION EXCHANGER ISOFOR	HYPOTHETICAL 33.3 KD P	THYROID HORMONE INDUCE
006319 Q95168 Q98708	051899	Q90491 Q18780 Q76660	082432 P97527	065813	092365	092872	030764 P96848	002839	014/68	015354	083101	060471	069681	091654
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                                                                    SEQUENCE
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MEDLINE; 98121113.

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ABGRAMP R., DIRKSE W., VAN STAVEREN M., STIEKEMA W., DROST L., BERGKAMP R., DIRKSE W., VAN STAVEREN M., TERRYN N., TEGHARNY A., AUEDORG S., GY I., KREIS M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P., RAITAN K.D., RIEGER M., SCHAEFFER M., FUNK B., MUBLLER AUER S., ROUFELATOUE E., MONTFORT A., PONS A., PUIGDOMENECH P., DOUKA A., VOUKELATOU E., MILIONI D., HATZOPOULOS P., PIRAYANDI E., OBERMAIER B., HILBERT H., DUESTERROFT A., MOORES T., JONES J.D.G., ENEVA T., ALLBERT H., DUESTERROFT A., MOORES T., JONES J.D.G., ENEVA T., RAILBERT H., VOET M., VOLCKAERT G., MEWES H.W., KLOSTERMAN S.,
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                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 74.6 KD PROTEIN.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                    120
                                                                             9
                                Gaps
 Gaps
                      MNPPFAKVSWATVTLLLLLLLLPPAVLSPGAAAQPLPDCCRQKTCSCRLYELLHGAGNHA
                                                                  AGILTLGKRRPGPPGLQGRLQRLLQASGNHAAGILTMGRRAGAEPAPRLCPGRRCLAAAA
                                                                                                                                                                                                                                                                                                                      BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L., POPESCU N.C., JOHNSON E.M. JR., MILBRANDT J.;
PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).
EMBL; AF051767; G2961632; --
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                                                                                                                                                                                                                                                                                                                                                                                        Score 113; DB 4; Length 400;
Pred. No. 5.76e-03;
 Indels
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SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                   (TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
 Mismatches 10;
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10;
                                                                                                                                                                                                                                         FAMILY RECEPTOR ALPHA 3.
                                                                                                                                                                                                        (TREMBLREL. 07,
                                                                                                                                                                                                                                                                                                                                                                                                     larity 47.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                          11.8%;
 Conservative
                                                                                                                                                                                  PRELIMINARY;
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nes 18; Conserv
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                                                                                                                                    120 TALAPRGG 127
                                                                                                               SSVAP-GG 127
                                                                                                                                                                                                       01-AUG-1998
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01-AUG-1998
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023352
023352;
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060609
060609;
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Matches
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SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                             598 KYCRSK-YETIHGONHDNAADVLELAIKREMPAELL-R-ASLRHTNEDORNFLLNVGRSA 654
                                                                                                                                                                                                                          Gaps
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STRAIN-SPRAGUE-DAMLEY; TISSUE-OSTEOSARCOMA;

MEDLINE; 93094223.

CHAN S.D.H., KARPF D.B., FOWLKES M.E., HOOKS M., BRADLEY M.S.,

VUONG V., BAMBINO T., LIU M.Y.C., ARNAUD C.D., STREWLER G.J.,

NISSENSON R.A.;

"I'MO homologs of the Drosophila polarity gene frizzled (fz) are

widely expressed in mammalian tissues.";

J. BIOL. CHEM. 267:25202-25207(1992).

-1- FUNCTION: MAY BE INVOLVED IN TRANSDUCTION AND INTERCELLULAR
                            of
                                                                                                                                                                                                                          4;
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SCHUELLER C., CHALWATZIS N.;
"Analysis of 1.9 Mb of contiguous sequence from chromosome 4
Arabidopsis thaliana.";
Arabidopsis thaliana.";
EMBL: 297337; E226841; -:
HYPOTHETICAL PROTEIN.
                                                                                                                                                                             Length 679;
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                                                                                                                                                                                                                        22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57B1/6;
MUNFORD R.S., FOSMIRE S., VARLEY A.W., STAAB J.F.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF018172; G2529571; ...
PFAM; PF00657; Lipase_GDSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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Pred. No. 4.90e-01;
                                                                                                                                                                               DB 10;
                                                                                                                                     B301B713 CRC32;
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                                                                                                                                                                               Score 106;
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                                                                                                                                     74635 MW;
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08,
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Best Local Similarity 38.18;
                                                                                                                                                                             Query Match 11.1%;
Best Local Similarity 32.3%;
Matches 20; Conservative
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01-NOV-1998 (TREMBLREL.
ACYLOXYACYL HYDROLASE.
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Job time : 42 secs
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SEQUENCE
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075779
075779;
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                                            SIGNAL.
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                                                                                                                                                                                                                                                                                                               RATTUS NORVEGICUS (RAT).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; PISUM.
                                                                                                                                                                                                                                                                                                                                                                                                              acyltransferase.";
BIOCHIM. BIOCHYS. ACTA 1346:207-211(1997).
-!- CATALYIIC ACTIVITY: PHOSCHATIDYLCHOLINE + STEROL = STEROL ESTER +
1-ACYLGLYCEROPHOSPHOCHOLINE.
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97166212.
PETERSEN C.M., NIELSEN M.S., NYKJAER A., JACOBSEN L., TOMMERUP N., RASMUSSEN H.H., ROIGAARD H., GLIEMANN J., MADSEN P., MOESTRUP S.K., "Molecular identification of a novel candidate sorting receptor
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY, AND WISTAR; TISSUE-LIVER;
MEDLINE; 97363611.
WANG J., GEBRE A.K., ANDERSON R.A., PARKS J.S.;
"Cloning and in vitro expression of rat lecithin:cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 440;
                                                                                                         Length 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                               4; Indels
                                          TISSUE=PERICARP;
RODRIGUEZ-CONCEPCION M., PEREZ-GARCIA A., BELTRAN J.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91; DB 11;
Pred. No. 3.45e+00;
2; Mismatches 5
                                                                                                        Score 92; DB 10;
Pred. No. 2.62e+00;
4; Mismatches 4
                                                                                   11828 MW; A45AD924 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49882 MW; 6CC16087 CRC32;
                                                                                                                                                                                                                    440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       833 AA.
                                                                                                                                                                                                                                                                                                                                      SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
                                                                                                                                                                                                                                      CREATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGLPGS--PWQWVLLLLGLLLPPA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U62803; G2306762; -.
PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNLPSTKVPWAAVTLLLLLLLPPA 24
                                                                                                                                                              72 ILLLLLPPPLLLLLMRPLPL 92
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03,
                                                                                                        Query Match 9.6%;
Best Local Similarity 61.9%;
Matches 13; Conservative
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Best Local Similarity 62.5%;
Matches 15; Conservative
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01-MAY-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                      01-JAN-1998 (TREMBLREL.
                                                                         EMBL; Z67873; E208986;
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                                                                                    106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 AA;
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                             SEQUENCE FROM N.A.
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035849
035849;
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Q99523
Q99523;
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EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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purified from human brain by receptor-associated protein affinity
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د
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SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Y15921; E1309800;
                                                                                                                                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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9
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Pred. No. 4.53e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89; DB 4; L
Pred. No. 5.93e+00;
                                                                                                         SORTILIN.
DOE351B9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDA
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UP
COLIAL AND PDGFB FUSION TRANSCRIPT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 144 14626 MW; AF87E707 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LQRLLHGDPGEEDGAELDLNMTRSHSGGELESLA-RGRR
                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Mismatches
                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                   10 WA-AVTLLLLL-LLPPALLSLG-VDAQPLP 36
                                                                                                                                                                                                                                              14 WPHGLGLLLLLQLLPPSTLSQDRLDAPPPP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: Fri Aug 20 21:03:02 1999
                 chromatography.";
J. BIOL. CHEM. 272:3599-3605(1997).
EMBL; X98248; E246784; -.
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                          33 PC
833 SC
92408 MW;
                                                                                                                                                                   Query Match 9.4%;
Best Local Similarity 53.3%;
Matches 16; Conservative
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Local Similarity 43.6%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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833 AA;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:01:51 1999; MasPar time 6.13 Seconds 599.747 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-938-548B-6 (1-130) from USO8938548B.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing:

summaries Minimum Match 0% Listing first 45

swiss-prot37 1:swissprot Database:

Mean 41.950; Variance 76.092; scale 0.551 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.07e-02 1.12e-02 1.12e-01 1.12e-01 1.12e-01 1.12e-01 1.12e-01 1.12e-01 1.12e-01 1.12e-01 1.12e-01 1.12e-01 1.13e-01 1.13e-01 1.13e-01 1.13e-01 1.05e+00 1.43e+00 1.45e+00 1.4	2.64e+00
Description	PLATELET GLYCOPROTEIN SECRETIN PRECURSOR (FR PHOSPHATIDY/CLOLINE-ST FIBULIN-1, ISOFORM A P FIBULIN-1, ISOFORM B P FIBULIN-1, ISOFORM C P FIBULIN-1, ISOFORM D PURPLET-PERIORECOMP PROSPHATIDY/CHOLINE-ST PHOSPHATIDY/CHOLINE-ST PHOSPHATIDY/CHOLINE-ST PHOSPHATIDY/CHOLINE-ST PROSTAGLANDIN G/H SYNT INFECTED CELL PROTEIN 4-1BB LIGAND (4-1BEL) SECI1 CYTOSOLIC FACTOR POGF-RELATED TRANSFORM INFECTED CELL PROTEIN INFECTED CELL PROTEIN REBOSOMAL LARGE SUBUNI FERRIC ENTEROBACTIN TR	PHOSPHATIDYLCHOLINE-ST
di di		LCAT_PAPAN
DB		-
Length	567 131 131 131 102 102 102 102 102 102 102 102 103 133 133 133 133 133 133 133 133 133	440
% Query Match		y .C
Score	H 1000000000000000000000000000000000000	αp
Result No.	14444444444444444444444444444444444444	73

	2.64e+00	2.64e+00	3.56e+00	3.56e+00	3.56e+00	3.56e+00	4.80e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00	6.46e+00							
	RETINAL GUANYLYL CYCLA	COMPLEMENT C3 PRECURSO	PLACENTAL LACTOGEN I P	PLATELET-DERIVED GROWT	HYPOTHETICAL 28 KD PRO	LIPASE 1 PRECURSOR (EC	LYSIS PROTEIN (E PROTE	LYSIS PROTEIN (E PROTE	EPHRIN-A3 PRECURSOR (E	LIPASE 3 PRECURSOR (EC	RIBOSOMAL LARGE SUBUNI	GIPASE ACTIVATING PROT	LUTROPIN-CHORIOGONADOT	PROTEIN-TYROSINE PHOSP	OXALATE OXIDASE PRECUR	SL CYTOKINE PRECURSOR	PUTRESCINE TRANSPORT S	PHOSPHATIDYLCHOLINE-ST	HYPOTHETICAL 59.6 KD P	PROTEIN-TYROSINE PHOSP	RETINAL GUANYLYL CYCLA	ANGIOTENSIN-CONVERTING
	CYGD_HUMAN	CO3_RAT	PLC1_BOVIN	PDGB_MOUSE	YPE1_RHORU	LIP1_PSYIM	VGE_BPPHX	VGE_BPS13	EFA3_HUMAN	LIP3_MORSP	RLUC_ECOLI	RN_DROME	LSHR_PIG	PTPX_MOUSE	OXO2_HORVU	FL3L_HUMAN	POTI_ECOLI	LCAT_RABIT	YABK_ECOLI	PTPX_RAT	CYGD_CANFA	ACE_RABIT
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•	86	98	82	82	82	82	84	84	84	84	84	84	84	84	83	83	83	83	83	83	83	83
	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                           CREATED)
                                                                                                                                                                                                                                                                                                       49765 MW;
                                                                                                                     SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                              EMBL; J05154; G293697; -.
                  STANDARD;
                                                                                                                                                                                                                                                              438
205
98
380
                                                                                                                                                                                                                                                                                44
108
296
397
408
                          01-AUG-1990 (REL. 15,
01-AUG-1990 (REL. 15,
01-NOV-1997 (REL. 35,
                                                                                                                                                                                                                                   EMBL; X54095; G52874;
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity (
                                                           MUS MUSCULUS (MOUSE)
                                                                                                                                                               ACT AS ACCEPTOR)
                                                                                                                                                                                                                                                                               44
108
296
397
408
438 AA;
                                                                            SEQUENCE FROM N.A.
                                                  ACYLTRANSFERASE)
             LT 3
LCAT_MOUSE
P16301;
                                                                                                                                                                                                                                                             CHAIN
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                           DISULFID
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14
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RESULT 4 ID FBLA_HUMAN REPEAT δ This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). MERONI G., MALGARETTI N., MAGNACHI P., TARAMELLI R.;
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS. CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL = STEROL ESTER + 1-ACYLGLYCEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CAN BE TRANSFERRED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN "Tissue-specific expression, developmental regulation, and chromosomal mapping of the lecithin: cholesterol acyltransferase gene. Evidence for expression in brain and testes as well as liver."; J. BIOL. CHEM. 264:21273-21581(1989). PIR; A34158; XXMSN. MGD; MGI:96755; LCAT. PROSITE: PS00120; IIPASE_SER; 1. TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL. SIGNAL ENZYME REGULATIÓN: APOLIPOPROTEIN A-1 IS A POTENT ACTIVATOR FOR THIS ENZYME. SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC, 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL LECITHIN-CHOLESTEROL ACYLTRANSFERASE. CHARGE RELAY SYSTEM (BY SIMILARITY). BY SIMILARITY. POTENTIAL. MEDLINE; 90094326. WARDEN C.H., LANGNER C.A., GORDON J.I., TAYLOR B.A., MCLEAN J.W. EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS. Score 96; DB 1; Length 438; Pred. No. 1.12e-01; 2; Mismatches 5; Indels POTENTIAL. 9E6B904A CRC32; 438 AA. TLLLLLLLPPALLSLGVDAOPLP 36 10.1%; larity 62.5%; Conservative

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24
1 MNLPSTKVPWAAVTLLLLLLLPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
-!- ALTERNATIVE PRODUCTS: FOUR FORMS OF FIBULIN-1; A (SHOWN HERE), E
(AC P23143), C (AC P23144) AND D (AC P37888); DIFFRRING ONLY IN
THEIR C-TERMINAL REGIONS, ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 3 ANAPHILATOXIN-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 8 COMPLETE AND ONE INCOMPLETE EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX; PLASMA; EGF-LIKE DOMAIN; CALCIUM-BINDING.
                                                                                                                                                                 MEDILINE; 8350-44.
MEDILINE; 8354537.
ARGRAVES W.S., DICKERSON K., BURGESS W.H., RUOSLAHTI E.;
"FIDULIN, a novel protein that interacts with the fibronectin
receptor beta subunit cytoplasmic domain.";
CELL 58:623-629(1989).
                                                                                                  EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBULIN-1, ISOFORM A.

3 X ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
                                    LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
 566 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS00010; ASX_HYDROXYL; 4.
PROSITE: PS00122; EGF_1; FALSE_NEG.
PROSITE: PS01177; ANAPHYLATOXIN_1; 3.
PROSITE: PS01178; ANAPHYLATOXIN_2; 3.
PROSITE: PS01186; EGF_2; 3.
PROSITE: PS01186; EGF_2; 3.
PROSITE: PS01086; EGF_5; 18.
PFAM; PF00008; EGF; 5.
HSSP; P35555; 1EMO.
                                                          FIBULIN-1, ISOFORM A PRECURSOR
                        20, CREATED)
20, LAST SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X53741; G31415; -.
 STANDARD;
                                                                                      HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A32826; A32826.
A36346; A36346.
                       01-NOV-1991 (REL. 01-NOV-1991 (REL.
                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 91100426.
                                                                                                                                                                                                                                 30-44
                                                01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30
36
37
77
77
1112
1112
2016
308
3356
441
441
525
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                                                                                                                                                                                                                                SEQUENCE OF
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Gaps

.; 7

MGLPGS -- PWQRVLLLLGLLLPPA 22

(POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL)

(POTENTIAL)

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GLYCOPROTEIN; EXTRACELLULAR MATRIX;
                                                              FIBULIN-1, ISOFORM C.

3 X ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 2, CALCIUM-BINDING (FEGF-LIKE 4, CALCIUM-BINDING (FEGF-LIKE 5, CALCIUM-BINDING (FEGF-LIKE 6, CALCIUM-BINDING (FEGF-LIKE 6, CALCIUM-BINDING (FEGF-LIKE 9, CALCIUM-BINDING (FEGF-LIKE 9
                                            DOMAIN; CALCIUM-BINDING
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PROSITE; PS01187; EGF_CA; 8.
PFRM; PF00008; EGF; 5.
HSSP; P35555; 1EMO.
SIGNAL; ALTERNATIVE SPLICING;
REPEAT; PLASMA; EGF-LIKE DOMAI
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Best Local Similarity 57.1%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 91100426.
ARGRAVES W.S., TRAN H., BURGESS W.H., DICKERSON K.;
FIDULIN is an extracellular matrix and plasma glycoprotein with repeated domain structure.";
J. CELL BIOL. 111:3155-3164(1990).
                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                              Score 96; DB 1; Length 601;
Pred. No. 1.12e-01;
3; Mismatches 8; Indels
                                                                                                                   S (IN REF. 2).
                                                                                                                               3A6E492B CRC32;
                                                                                                                                                                                                                                                                                           01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBULIN-1, ISOFORM C PRECURSOR.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
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C -> S (IN
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PIR; C36346; C36346.

MIM; 135820; PROSITE; PS00010; ASX_HYDROXXL; 4.

PROSITE; PS00022; EGF_1; FALSE_NEG.

PROSITE; PS01177; ANAPHYLATOXIN_1; 3.

PROSITE; PS01178; ANAPHYLATOXIN_2; 3.

PROSITE; PS011186; EGF_2; 3.
                                                                                                                                                                                                         10 VPLPLLLLGGLALLAAGVDADVLLEACC 37
                                                                                                                                                                                                                      HR
                                                                                                                                           M.
                                                                                                                                                              Match 10.1%;
Local Similarity 57.1%;
Les 16; Conservative
                                                                                                                                          65485
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  J. CELL BIOL. 111:3
[2]
SEQUENCE OF 30-44.
                                                                                                                                          601 AA;
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FBLC_HUMAN
P23144;
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Mismatches 8;
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67EFDOD6 CRC32;
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01-NOV-1990
                                               01-NOV-1990
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LCAT_RAT
P18424;
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                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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LOS. TRANS. R. SOC. LOND., B, BIOL. SCI. 306:345-354(1984).
FUNCTION: C10 ASSOCIATES WITH THE PROBNIZMES CIR AND C1S TO YIELD
C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE
COLLAGEN-LIKE REGIONS OF C10 INTERACT WITH THE CA(2+)-DEPENDENT
C1R(2)C1S(2) PROBNIZME COMPLEX, AND EFFICIENT ACTIVATION OF C1
FAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE
FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEXES.
SUBUNIT: C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF
WHICH ARE DISULFIDE-LINKED DIMERS OF THE A & B CHAINS, AND THREE
                                                                                                                                                                                                                                         PROSITE; PS01113; C1Q; 1.
PFAM; PF00386; C1q; 1.
COMPLEMENT PATHWAY; PLASMA; HYDROXYLATION; GLYCOPROTEIN; COLLAGEN;
                                                                                                                                                                                                                                                                                                                          (WITH CYS-26 IN CHAIN A).
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Pred. No. 5.61e-01;
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N REF. 2).
N REF. 2 AND 3).
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HYDROXYLATION.
GLUCOSYLGALACTOSE.
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                                                                                                                                                                                                        EMBL; M36278; G179638; -.
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PIR; B23422; B23422.
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Matches 8; Consei
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  PHILOS.
                                                                                                                                                                                                                                                                               SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                  MERONI G., MALGARETTI N., MAGNAGHI P., TARAMELLI R.;
"Nuclectide sequence of the cDNA for lecithin-cholesterol acyl
transferase (LCAT) from the rat.";
NUCLEIC ACIDS RES. 18:5308-5308(1990).
-!- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
LIPORROTEINS. AMONG OTHERS SUBSTRATES IT ESTERIES THE FREE
CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
-!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL = STEROL ESTER +
1-ACYLGLYCEROPHOSPHOCHOLINE (PALMITOYL, OLDSYL, AND LINDLEOYL CAN
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TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                            01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
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CHARGE REILA.
BY SIMILARITY.
BY SIMILARITY.
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
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(REL. 34, LAST ANNO
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90384859.
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                                                                                                                                                                       ACYLTRANSFERASE)
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LCAT_HUMAN
P04180;
20-MAR-1987 (
20-MAR-1987 (
01-OCT-1996 (
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SEQUENCE FROM N.A. MEDLINE; 87217119.
 SEQUENCE FROM N.A.
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                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       MEDLINE; 85296313
                                                                                                     MEDLINE; 86205961
                                                                                                                                                                                84205633
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 85269623
                                                                                                                                                                                                         AARONSON S.A.;
                                 WONG-STAAL F
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                              HUM. MUTAT. 8:79-82(1996).

-!- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.

-!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL = STEROL ESTER + 1-ACYLGLYCEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEGYL CAN BE TRANSFERRED: A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
"Complete deficiency of plasma lecithin-cholesterol acyltransferase (LCAI) activity due to a novel homozygous mutation (Gly-30-Ser) in
                                                                                                             ACT AS ACCEPTOR). ENZYME REGULATION: APOLIPOPROTEIN A-1 IS A POTENT ACTIVATOR FOR
                                                                                                                                                                      -!- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                 DISEASE: DEFECTS IN LCAT ARE THE CAUSE OF NORUM AND FISH EYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
PDGF-2) (BACAPLERMIN).
PDGFB OR C-SIS.
HOMO SAPIENS (HUMAN).
PURARYOTA: METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 1; Length 440; Pred. No. 5.61e-01;
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                                                                                                                                                                                LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AA.
                                                                                                                                                                                                                                                                                                          EMBL; X06537; -; NOT_ANNOTATED_CDS.
EMBL; M2658; GB7025; -
EMBL; X04981; G34287; -
EMBL; M17959; G386858; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: remainder of annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE MUTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDGB_HUMAN STANDARD; F
P01127; P78431;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQI
15-DEC-1998 (REL. 37, LAST ANNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.5%;
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205
98
380
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108
296
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PIR; A29661; A29661.
PIR; A25575; A25575.
PIR; JQ0036; JQ0036.
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Matches 13; Conser
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205
74
337
                                                                                                                                      THIS ENZYME
                     the LCAT gene.
HUM. MUTAT. 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYMORPHISM;
                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 136120;
MIM; 245900;
                                                                                                                                                           DISEASES
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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MEDLINE, 97141927.
SIMON M.-P., PEDEUTUUR F., SIRVENT N., GROSGEORGE J., MINOLETTI F., COINDRS J.-M., TERRIER-LACOMER M.-J., MANDALL N., CRAVER R.D., BLIN N., SOZZI G., TURC-CAREL C., O'BRIEN K.P., KEDRA D., FRANSSON I., GUILBAUD C., DUMANSKI J.P.; Deregulation of the platelet derived growth factor B-chain gene via
                                                                                    WONG-STAAL F.;
"Transforming potential of human c-sis nucleotide sequences encoding platelet-derived growth factor.";
SCIENCE 225:636-639(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans and giant-cell fibroblastoma.";
NAT. GENET. 15:95-98(1997).
                                                                                                                                                                                                                                                                                                                                                RAO C.D., IGARASHI H., CHIU I.-M., ROBBINS K.C., AARONSON S.A.; STRUCTURE and sequence of the human c-siz/platelet-derived growth factor 2 (SIS/PDGF2) transcriptional unit.", PROC. NATL. ACAD. SCI. U.S.A. 83:2392-2396(1986).
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WEICH H.A., SEBALD W., SCHAIRER H.U., HOPPE J.;
"The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase mrna which codes for the sequence of the PDGF-B chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLINS T., GINSBURG D., BOSS J.M., ORKIN S.H., POBER J.S.; "Cultured human endothelial cells express platelet-derived growth factor B chain: cDNA cloning and structural analysis."; NATURE 316:748-750(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WONG-STAAL F.;
CDNA clones with
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G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth
MEDLINE; 84250225.
JOSEPHS S.F., RAINER L., CLARKE M.F., WESTIN E.H., REITZ M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -M., REDDY E.P., GIVOL D., ROBBINS K.C., IRONICK S.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence analysis identifies the human c-sis
proto-oncogene as a structural gene for platelet-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 84236121.
JOHNSSON A., HELDIN C.H., WASTESON A., WESTERMARK B.,
HUANG J.S., SEBBURG P.H., GRAY A., ULLRICH A., SCRACE
STROOBANT P., WATERFIELD M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The c-sis gene encodes a precursor of the B chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLD SPRING HARB. SYMP. QUANT. BIOL. 51:959-966(1986)
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SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 153-200 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RATNER L., JOSEPHS S.F., JARRETT R., REITZ M.S., "Nucleotide sequence of transforming human c-sis homology to platelet-derived growth factor."; NUCLEIC ACIDS RES. 13:5007-5018(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 26-241 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 22-241 FROM N.A. MEDLINE; 84205633.
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BIOCHEM. BIOPHYS. 307:361-368(1993).
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106
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339
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ACT_SITE
BINDING
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CARBOHYD
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                                                                                                                                                                                                                                      SAITOH E., ISEMURA S., SANADA K.; "Further fractionation of basic proline-rich peptides from human parotid saliva and complete amino acid sequence of basic proline-rich peptide P-H."; J. BIOCHEM. 94:1991-1997/1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGH1_RAT

DGG31; Q6231; Q6284;

Q63921; Q6231; Q6384;

15-DEC-1998 (REL. 37, CREATED)

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

16-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

17-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

18-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

19-DEC-1998 (REL. 37, LAST ANNOTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MILILLSVALLALS-SAQNINEDVSQEE-S-P--SLIAGNP-QGPSPQG-GNKPQGPPPP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                            KAUFFMAN D., HOFMANN T., BENNICK A., KELLER P.; "Basic proline-rich proteins from human parotid saliva: complete covalent structures of proteins IB-1 and IB-6."; BIOCHEMISTR 25:2387-2392(1986).
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 89; DB 1; Length 331;
Pred. No. 1.05e+00;
26; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT; PAROTID GLAND; MULTIGENE FAMILY; SALIVA; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDE IB-6.
PEPTIDE P-H.
MISSING (IN CLONE CP-4).
MISSING (IN CLONE CP-5).
A -> S (IN REF. 2 AND 3).
W; D18DE589 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32596 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K03204; G190486; -. EMBL; K03205; G190504; -. EMBL; K03206; G190506; -.
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238
258
276
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EUKARYOTA; METAZOA; CH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 94099619.
                    SEQUENCE OF 214-331.
MEDLINE; 86243355.
KAUFFMAN D., HOFMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A03291; PIHUB6.
PIR; C25372; C25372.
MIM; 168730; -.
                                                                                                                                                                                                                             SEQUENCE OF 276-331.
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331 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE.
-!- THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE.
-!- THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS SUCH AS ASPIRIN.
                                                                                                                                                                                                                                                                        -! - CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2, O(2) = PROSTAGLANDIN
SEQUENCE FROM N.A.
STRAINFISHER 344; TISSUE-TRACHEA;
MEDLINE; 95168876.
KITZLER J., HILL E., HARDMAN R., REDDY N., PHILPOT R., ELING T.E.;
"Analysis and quantitation of splicing variants of the TPA-inducible PGHS-I mRNA in rat tracheal appthenial cells.";
ARCH. BIOCHEM. BIOCHEM. 316:856-863(1995).
-! FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING OR PROMOTING CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISTAL HISTIDINE (BY SIMILARITY).
CYCLOOXYGENASE (BY SIMILARITY).
PROXIMAL HEME LIGAND (BY SIMILARITY).
ASPIRIN-ACETYLATED SERINE.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                      H2 + A + H(2)O.
-!- PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
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EMBL; S67721; G466556; -
EMBL; U18060; G603052; -.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
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Best Local Similarity 40.0%;
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:01:12 1999; MasPar time 8.58 Seconds 607.078 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-6 (1-130) from USO8938548B.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATALALAPRGGSRV 130

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 40.689; Variance 84.298; scale 0.483 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.96e-02	9.12e-02	1.23e-01	2.25e-01	4.07e-01	4.07e-01	4.07e-01	9.78e-01	9.78e-01	1.74e+00	1.74e+00	1.74e+00	1.74e+00	3.06e+00	3.06e+00	3.06e+00	3.06e+00	3.06e+00	3.06e+00	4.05e+00	4.05e+00	4.05e+00	4.05e+00
Description	hypothetical protein	secretin precursor -	catalase (EC 1.11.1.6	probable intercellula	phosphatidylcholine	fibulin 1 precursor,	fibulin 1 precursor,	collagen alpha chain	natriuretic peptide r	complement subcompone	phosphatidylcholine	phosphatidylcholine	cyclooxygenase 1 - ra	hypothetical protein	platelet-derived grow	platelet-derived grow	salivary proline-rich	prostaglandin G/H syn	cal prote	probable cutinase pre	ligand (4-1BB ligand - human	stromelysin 3 (EC 3.4
ID	C71413	SEPG	JA0091	A45054	XXMSN	B36346	C36346	S28774	OYHUAR	ClHUQB	XXRIN	XXHUN	S39782	S58383	A55030	PFHUG2	PIHUB6	86168	T00382	A70565	S43293	84	JC6197
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Length	619	131	495	641	438	601	683	1027	1061	253	440	440	602	185	230	241	392	602	1321	226	245	254	491
% Query Match	11.1	10.6	10.5	10.3	10.1	10.1	10.1	7.6	7.6	9.5	9.5	9.5	9.5	9.3	9.3	9.3	9.3	9.3	٠	٠	9.5		9.5
Score	106	101	100	86	96	96	96	93	93	91	91	91	91	68	68	ъ 8	68	68	σ σ	88	88	88	88
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598 KYCRSK-YETIHGQNHDNAADVLELAIKREMPAELL-R-ASLRHTNEDQRNFILLNVGRSA 654

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9.24e+00 1.21e+01 1.21e+01 1.21e+01 1.21e+01 3e-ear	hypothetical protein 9.24e gene E protein - phag 1.21e lutropin-choriogonado 1.21e lutropin-choriogonado 1.21e lutropin-choriogonado 1.21e TS te te Arabidopsis thaliana s thaliana #common name mouse-ear	2 T00728 hypoth 2 J50455 gene E 2 B41344 lutrop 2 C41344 lutrop 2 C41344 lutrop ALIGNMENTS ALIGNMENTS #type complete I protein - Arabidopsis e Arabidoosis thallana	4 00000	915 91 329 331 331 etica	8.9 8.8 8.8 8.8 8.8 C71413 hypothe	884 884 1	41 42 43 44 45 45 ENTRY ENTRY ORGANISM
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	endothelin receptor t	JC5501	0	613.	o.	82	40
9.24e+00	probable nhow protein	D70605	4 (7	332	0.00	82	0 0 0 0
	triacylglycerol lipas	S57275	01	317	8 G	82	37
	hypothetical protein	S12255	7	255	8.0	82	36
	platelet-derived grow	PFMSGB	Н	241	8.9	82	35
9.24e+00	placental lactoden pr	A37930	7	236	8.9	85	34
7.03e+00	complement C3 precurs	C3RT	٦.	1663	0.6	86	33
7.03e+00	quanylate cyclase (EC	JH0717	(7)	1102	0.6	86	32
7.03e+00	phosphatidylcholine	JC1502	4 (4	440	0.0	8 8	
7.03e+00	hypothetical protein	G64151	~	322	0.0	9 0	500
5.34e+00	prostaglandin-endoper	A36746	7	299	9.1	87	28
5.34e+00	Ω	150518	7	583	9.1	87	27
		A25669	7	271	9.1	87	26
5.34e+00	PDGF-related transfor	TVMVSS	Н	226	9.1	87	25
4.05e+00	phosphatidylinositol-	S43745 ·	7	497	9.5	88	24

C71413 #type complete hypothetical protein - Arabidopsis thaliana #formal_name Arabidopsis thaliana #common_name mouse-ear cress columbia 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-per-1998	A71413 A71400 Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirkse, W.; Van Staveren, M.; Stiekema, W.; Drost, L.; Ridley, P.; Hudson, S.A.; Patel, K.; Murphy, G.; Piffanelli, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Gielen, J.; Villarroel, R.; De Clerck, R.; Van Montaqu, M.; Lecharny, A.; Auborg, S.; Gy, I.; Kreis, M.; Lao, N.; Kavanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Punk, B.; Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, P.; Douka, A.; Voukelatou, E.; Milioni, D.; Hatzopoulos, P.; Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny, W. Vock, M.; Vock, R.; Berger, C.; Delseny,	Na An erence C7	_type DN 1- ferences 4COP9-4 #length	Query Match 11.1%; Score 106; DB 2; Length 679; Best Local Similarity 32.3%; Pred. No. 1.96e-02; Matches 20; Conservative 16; Mismatches 22; Indels 4; Gaps 4;
RESULT 1 ENTRY TITLE ORGANISM #variety DATE	ACCESSIONS REFERENCE #authors	#journal #title #cross-refe #accession #*status	##molecule ##residues ##cross-re GENETICS #map_position SUMMARY	Query Match Best Local S Matches

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#Journal J. Biol. Chem. (1989) 264:21573-21581

#title Tissue-specific expression, developmental regulation, and chromosomal mapping of the lecithin:cholesterol acyltransferase gene. Evidence for expression in brain and testes as well as liver.
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Meroni, G.; Malgaretti, N.; Magnaghi, P.; Taramelli, R.
submitted to the EMBL Data Library, July 1990
Promoter and 5' flanking sequences of the mouse LCAT gene.
S21370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasma glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #product phosphatidylcholine--sterol acyltransferase
#status predicted #label MAT\
#binding_site carbohydrate (Asn) (covalent) #status
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K. J. Gell Biol. (1990) 111:3355-3164 Fibulin is an extracellular matrix and plasma glycoprowith repeated domain structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
#length 438 #molecular-weight 49765 #checksum 1794
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Pred. No. 4.07e-01;
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#map_position 22q13.3-22q13.3
CLASTETCATION #superfamily EGF homology
KEYWORDS alternative splitcing
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                            A34158; S21370
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENETICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
ENTRY
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Argraves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E. Cell (1989) 58:623-629
Fibulin, a novel protein that interacts with the fibronectin receptor beta-subunit cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
J. Cell Biol. (1990) 111:3155-3164
Fibulin is an extracellular matrix and plasma glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain signal sequence #status predicted #label SIG\
#product fibulin 1 splice form C #status predicted
#label MAT\
#binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name Homo sapiens #common_name man
19.Apr-1991 #sequence_revision 19-Apr-1991 #text_change
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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#length 683 #molecular-weight 74475 #checksum 7443
                                                                                                                                                                                                                                                                                                                                                                                      fibulin 1 splice form A; fibulin 1 splice form C
                           #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.1%; Score 96; DB 2; Length 683; Best Local Similarity 57.1%; Pred. No. 4.07e-01; Matches 16; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 601
4.07e-01;
                                                                                                                                                                                                                                                                                                              C36346 #type complete
fibulin 1 precursor, splice form C - human
fibulin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-683 ##label ARG
##cross-references GB:X53743; NID:g31418; PID:g31419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
##residues 1-566 ##label AR2
##cross-references GB:X53741; NID:g31414; PID:g31415
#domain EGF homology #label EGF
#length 601 #molecular-weight 65485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references GDB:278285; OMIM:135820
#map_position 22q13.3-22q13.3
KEYWORDS alternative splicing; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with repeated domain structure.
#cross-references MUID:91100426
                                                                                                                    3; Mismatches
                                                                     Score 96;
Pred. No.
                                                                                                                                                                   10 VPLPLLLGGLALLAAGVDADVLLEACC 37
                                                                                                                                                                                            10 VPLPLLLGGLALLAAGVDADVLLEACC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-Sep-1997
C36346; A36346; A32826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cross-references MUID:89354537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDB: FBLN1; FBLN
                                                                                           Best_Local Similarity 57.1%;
Matches 16; Conservative
                                                                     10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
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GENETICS

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Reid, K.B.M.; Thompson, E.O.P.
Biochem. J. (1978) 173.863-868
Amino acid sequence of the N-terminal 108 amino acid residues of the Behin of subcomponent Clq of the first component of human complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The first component of complement is a calcium-dependent complex of the three subcomponents Clq, Clr, and Cls. Subcomponent Clq binds to immunoglobulin complexes, with resulting serial activation of Clr (enzyme), Cls (proenzyme), and the other eight components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #Eross-references GDB:119043; OMIM:120570
#map_position 1p36.3-1p34.1
CLASSIFICATION #superfamily complement subcomponent Ciq chain A; complement Clq carboxyl-terminal homology
KEYWORDS complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyproline; plasma; pyroglutamic acid; triple helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #product complement subcomponent Clq chain B #status
experimental #label MATN
#Commain collagenous, triple helix #label COL\
#domain complement Clq carboxyl-terminal homology #label
                                                                                                                                                                                                                                                                                                                                       Reid, K.B.M.; Gagnon, J.; Frampton, J.
Bloochen. J. (1982) 203:559-569
Completion of the amino acid sequences of the A and B chains
of subcomponent Clq of the first component of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXTN #type complete
phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #modified_site pyrrolidone carboxylic acid (Gln) (ir
mature form) #status experimental\
#disulfide_bonds interchain (to chain A-26) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          experimental\
#binding_site carbohydrate (Lys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #length 253 #molecular-weight 26722 #checksum 7399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Cig subcomponent is composed of nine subunits, six of disulfide-linked dimers of the A (see PIR:CHHUQA) and B and three of which are disulfide-linked dimers of the C PIR:CHHUQC) chain. Equimolar amounts of the A, B, and C are found after reduction of the disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #modified_site 4-hydroxyproline (Pro) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #modified_site 5-hydroxylysine (Lys) #status
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  'E',29-84,'D',86-99,'P',101-135 ##label
                                                                                                                                                                                                                                                 ##molecule_type protein
##residues 28-99,'P',101-195 ##label RE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176-Glx may also be present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type protein
##residues 136-253 ##label RE4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #cross-references MUID:82283890
                                                                                                                                                                                                   #cross-references MUID:79041552
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Local Similarity 53.3%;
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement
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                               A90301
                                                                                                                                                                                                                                                                                                             A90315
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     ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##note
                                                         #authors
#journal
#title
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                               REFERENCE
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#title Molecular cloning and characterization of the complementary
DNA and gene coding for the B-chain of subcomponent Clq of
the human complement system.
#cross-references MJID:86076906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions present in subcomponent Clq of the first component of human complement.
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                                             #gene GDB:NPR1; NPRA; ANPRA #seross-references GBB:125199; OMIM:108960 #map_position 1q21-1q22 GBB:125199; OMIM:108960 #map_position 1q21-1q22 CLASSIFICATION #superfamily membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homology; natriuretic peptide-binding domain homology; protein kinase homology XEXWORDS ATP; carbon-oxygen lyase; cGPM biosynthesis; glycoprotein; hormone receptor; phosphorus-oxygen lyase; transmembrane
                                                                                                                                                                                                                                                                                                                                       #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'HS',1-32 ##label REI
the authors translated the codon AGT for the second
position as Arg; they were uncertain about the
location of the initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J. (1979) 179:367-371
Complete amino acid sequences of the three collagen-like
                                                                                                                                                                                                                                                                                                                                                              *product natriurefic peptide receptor A *status
predicted *label MAT\
#Gomain extracellular *status predicted *label EXT\
#Gomain natriuretic peptide-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain transmembrane #status predicted #label TMMN, #domain intracellular #status predicted #label INTN, #domain protein kinase homology #label KINN #domain guanylate cyclase catalytic domain homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C1HUQB #type complete complement subcomponent C1g chain B precursor - human complement subcomponent C1g beta chain #formal_name Homo sapiens #common_name man 22-May-1981 #sequence_revision 31-May-1996 #text_change
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#length 1061 #molecular-weight 118918 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.7%; Score 93; DB 1; I
larity 48.6%; Pred. No. 9.78e-01;
Conservative 6; Mismatches 10
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##residues 28-253 ##label RE1
##cross-references EMBL:X03084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #label NPB\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #label CAT\
##experimental_source retina
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##molecule_type protein
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nes 17; Conser
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386,427
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RESULT

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Matches

SUMMARY

tauthors

#authors #journal

REFERENCE

ACCESSIONS REFERENCE

ORGANISM

495-1061 526-808

474-494

828-1055

33-473 113-453

1-32 33-1061

FEATURE

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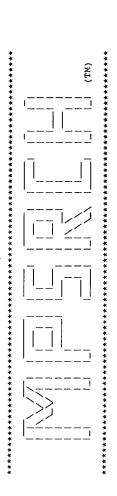
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Gaps

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Search completed: Fri Aug 20 21:01:34 1999 Job time : 22 secs.
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SUMMARY
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                                                                                                                                       catalyzes the transfer of sn-2 fatty acyl groups from phosphatidylcholine (lecithin) to sterol to form sterol fatty esters and lacylglycerphosphocholine palmitcyl, oleoyl, and linoleoyl residues can be transferred; a number of sterols, including cholesterol, can act as
                                                                                                                                                                                                                                                                      #superfamily phosphatidylcholine--sterol acyltransferase
acyltransferase; cholesterol; glycoprotein; lipid metabolism;
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Apolipoprotein A-I (see PIR:LPHUA1) is a potent activator of this
                                                                                                                                                                                                                                                                                                                                                   #domain signal sequence #status predicted #label SIG(
#product phosphatidylcholine--sterol acyltransferase
#status experimental #label MAT(
#status experimental #label MAT(
#binding_site carbohydrate (Asn) (covalent) #status
experimental(
#binding_site carbohydrate (Thr) (covalent) #status
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#binding_site carbohydrate (Thr) (covalent) #status
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#binding_site carbohydrate (Ser) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #formal_name Rattus norvegicus #common_name Norway rat 20-May-1994 #sequence_revision 10-Nov-1995 #text_change 29-Jan-1999 $33782 $39782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $58383  #type complete
hypothetical protein 2 - human
#formal_name Homo sapiens #common_name man
12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
02-Jul-1998
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#Emolecule_type mRNA
##molecule_type mRNA
##residues 1-602 ##label FEN
##cross-references GB:S67721; NID:9460555; PID:9460556
##cross-references GB:S67721; NID:9460555; PID:9460556
##cross-references GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         experimental #length 440 #molecular-weight 49578 #checksum 8696
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Pred. No. 1.74e+00;
0; Mismatches 3; Indels
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                                                                        ##cross-references GDB:119359; OMIM:245900
#map_position 16q22.1-16q22.1
FUNCTION
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Best Local Similarity 40.0%;
Matches 16; Conservative
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Local Similarity 81.3%;
les 13; Conservative
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##cross-references GB:X00556; GB:X00559; GB:X00560; GB:X00561; GB:X00562 FICATION #superfamily platelet-derived growth factor #length 230 #checksum 3580
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Deuel, T.F.; Huang, J.S.; Seeburg, P.H.; Gray, A.; Ullrich,
A.; Scrace, G.; Stroobant, P.; Waterfield, M.D.
EMBO J. (1984) 3:921-928
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Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
Nucleic Acids Res. (1995) 23:2815-2822
A novel human c-sis mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.
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platelet-derived growth factor chain B precursor - human
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18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change
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                                                                                                                                                                              ##status preliminary
##molecule_type mRNA
##molecule_type mRNA
##residues 1-185 ##label DIR
##cross-references FMBL:X83705; NID:9951023; PID:9951025
CLASSIFICATION #superfamily platelet-derived growth factor
SUMMARY #length 185 #molecular-weight 20774 #checksum 2728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The c-sis gene encodes a precursor of the B chain of platelet-derived growth factor.
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LQRLLQAN-GNH-AAGI-LIMGR-RAGAELEPYPCPGRR 113
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Pred. No. 3.06e+00;
11; Mismatches 6
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9.3%;
Best Local Similarity 43.6%;
Matches 17; Conservative
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Best Local Similarity 43.6%;
Matches 17; Conservative
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:04:31 1999; MasPar time 2.87 Seconds 459.570 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-6 (1-130) from US08938548B.pep 954

Description: Perfect Score: Sequence: Title:

1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATALAPRGGSRV 130

PAM 150 Gap 11 Scoring table:

Searched:

106580 seqs, 10152877 residues

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Database:

Mean 28.030; Variance 126.736; scale 0.221 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Pred	7.6	1.2	1.2	1.2	1.4	1.7	1.7	1.7	1.7	2.4	2.4	2.4	•	2.8	•	2.8	2.8		ω,	3.3	ص 9.	5.5	5.5
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	Desc	Patent	Sedu	Patent	Sedn	Sedu	Patent	Patent	Patent	Sedu	Sedu	Sedu	Sedu	Sedu	Sequ	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Patent	Sedu	Sedu
	ID	5175255-4	PCT-US96-0	5194596-15	US-08-387-	US-08-236-	5498600-2	5175255-2	5175255-8	US-08-445-	US-08-469-	PCT-US94-1	US-08-465-	•	US-08-299-	US-08-453-	US-08-240-	US-08-026-	US-08-243-	PCT-US94-0	US-08-993-	5219739-15	US-07-794-	US-08-001-
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TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
                                                                                                                                                                                                                             APPLICANT: Thomason, Arlen R.;Nicholson, Margery
TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
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Pred. No. 1.76e+01;
11; Mismatches 6; Indels
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 Query Match 9.1%; Score 87; DB 4; Ler
Best Local Similarity 43.6%; Pred. No. 1.76e+01;
Matches 17; Conservative 11; Mismatches 6;
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79 LQRLLQAN-GNH-AAGI-LTMGR-RAGAELEPYPCPGRR 113
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
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CE 261 AA; 29370 MW; 369384 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5498600

APPLICANT: WIRRAY, MARK J.;KELLY, JAMES D.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOSAIC PROTEINS
NUMBER OF SEQUENCES: 34

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,776

FILING DATE: 07-0CT-1994

PRIOR APPLICATION NUMBER: 379,239
FILING DATE: 11-7U1-1989

C APPLICATION NUMBER: 379,239
FILING DATE: 11-7U1-1989

C APPLICATION NUMBER: 941,970
FILING DATE: 11-5-DEC-1986

C APPLICATION NUMBER: 941,970
FILING DATE: 15-DEC-1986

C APPLICATION NUMBER: 896,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 88; DB 1; Length 254;
Pred. No. 1.49e+01;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 87; DB 4; Length 226;
Pred. No. 1.76e+01;
11; Mismatches 6; Indels
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AA
                                                            APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
                                                                         FILING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                     NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERNCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE 254 AA; 26624 MW; 316872 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 AA; 27563 MW; 324570 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 705,175
FILLING DATE: 25-FEB-1985
APPLICATION NUMBER: 660,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                       : 254 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-OCT-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 3-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.2%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.1%;
Best Local Similarity 43.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 LPWALVAGLLLLLLAAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||| |: ||||||::|
8 VPWAAVT-LLLLLLPPA 24
                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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1 MNLPSTKVPWAAVTLLLLLLLLPPALLSLGVDAQPLPDCCRQKTCS 45
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                                                                                                        STANDARD;
                                                                            RESULT 13

AC XXXXX

AC XXXXXX

DT XX Sequence 3, Applic XX

XX Sequence 3, Applic C SENERAL INFORMAT SHAPLICANT: RAPLICANT: RAPLICA
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US-08-299-567-5
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                                                                                                                                                                             Score 85; DB 3; Length 613;
Pred. No. 2.44e+01;
13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 613;
                                                                                                                                                                                                                                                                                1 MRAPGALLARMSRLLLLLLLKVSASSALGVAPASRNETCLGESCA 45
                                                                                                                                                                                                                                                                                                             1 MRAPGALLARMSRLLLLLLKVSASSALGVAPASRNETCLGESCA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Endothelin Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: CARELLA, BYRNE, BAIN, GILFILLAN, E: CECCHI, STEWART & OLSTEIN 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325800-322 (PF137)
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Pred. No. 2.44e+01;
13; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,687A
FILING DATE: 6 JUNE 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US94/11843
FILING DATE: 17 OCT 1994
ATTORNEY/AGENT INFORMATION:
                                               STRANDEDNESS:
TOPOLOGY: LINBAR
MOLECULE IYPE: PROTEIN
JENCE 613 AA; 67034 MW; 1960405 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ENCE 613 AA; 67034 MW; 1960405 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08465687A
Patent No. 5750370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08465687A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 2:
: 613 AMINO ACIDS
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 613 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: P
                                                                                                                                                                             Query Match
Best Local Similarity 31.1%;
Matches 14; Conservative
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Best Local Similarity 31.1%;
Matches 14; Conservative
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: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ROSELAND
STATE: NEW JERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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ADDRESSEE:
STREET: 6 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
  LENGIH:
                                                                                                                             SEQUENCE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 CRL-YE-LLHGAGNHAAGILTIGKRRPGPPGLQGRLQRLLQA-NGNHAAGIL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 954;
                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
8.9%; Score 85; DB 2; L
Best Local Similarity 40.4%; Pred. No. 2.44e+01;
Matches 21; Conservative 9; Mismatches 16
                                                             APPLICANT: RACIE, Lisa
APPLICANT: LaVALLIE, Edward
APPLICANT: DeROBERTIS, Edward
TITLE OF INVENTION: CHORDIN COMPOSITIONS
WUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       E: Genetics Institute, Inc. 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/749,169A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
FINCE 954 AA; 101960 MW; 4424673 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
Sequence 3, Application US/08749169A
Patent No. 5846770
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08299567
Patent No. 5747033
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAGAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI STELECOMMUNICATION INFORMATION:
TELEPHONE: (617),498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08299567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,618
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 954 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Davis, et al.
                                                                                                                                                                                                                             CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT ID US
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 3.32 Seconds 280.825 Million cell updates/sec Fri Aug 20 21:06:48 1999; Run on:

Tabular output not generated.

>US-08-938-548B-8 (1-33) from US08938548B.pep 256 1 QPLPDCCRQKTCSCRLXELLHGAGNHAAGILTL 33 Title:

Description: Perfect Score: Sequence:

77977 seqs, 28268293 residues PAM 150 Gap 11 Searched:

Scoring table:

summaries Minimum Match 0% Listing first 45 Post-processing:

1:swissprot swiss-prot37 Database:

Mean 31.702; Variance 45.079; scale 0.703 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		œ			SUMMARIES		
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No.
	75	29.3	373	<u>.</u>	ICEB MOUSE	CASPASE-11 PRECURSOR (5.93e-02
7	73	28.5	260	Н	NMA_HUMAN	PUTATIVE TRANSMEMBRANE	1.38e-01
٣	72	28.1	815	, -	GYRB_MYXXA	DNA GYRASE SUBUNIT B (2.10e-01
4	71	27.7	413	-	PPAW_CAEEL	PUTATIVE ACID PHOSPHAT	3.18e-01
Ŋ	70	27.3	214	-	R10A_TRYBR	60S RIBOSOMAL PROTEIN	4.80e-01
9	69	27.0	197	1	MCS_MOUSE	SPERM MITOCHONDRIAL CA	7.21e-01
7	69	27.0	461	 1	YUL2_CAEEL	PUTATIVE FORKHEAD-RELA	7.21e-01
∞	89	26.6	641	~	TETS_LISMO	TETRACYCLINE RESISTANC	1.08e+00
δ	68	26.6	646	Н	TETS_LACLA	TETRACYCLINE RESISTANC	1.08e+00
10	67	26.2	299	Н	ALC_RABIT	IG ALPHA CHAIN C REGIO	1.61e+00
11	67	26.2	923	Н	RE11_SCHPO	MEIOTIC RECOMBINATION	1.61e+00
12	99	25.8	347	~	GALE_RAT	UDP-GLUCOSE 4-EPIMERAS	2.38e+00
13	99	25.8	348		GALE_HUMAN	UDP-GLUCOSE 4 - EPIMERAS	2.38e+00
14	99	25.8	360		PURK_PSEAE	PHOSPHORIBOSYLAMINOIMI	2.38e+00
15	99	25.8	380	7	LEU3_PHACH	3-ISOPROPYLMALATE DEHY	2.38e+00
16	99	25.8	425	Н	IFI5_MOUSE	INTERFERON-ACTIVATABLE	2.38e+00
17	65	25.4		-	Y115_METJA	HYPOTHETICAL PROTEIN M	3.52e+00
18	65	25.4	7	Н	MD12_SCHPO	MITOCHONDRIAL INHERITA	3.52e+00
19	64	25.0		7	TX03_AGEAP	OMEGA-AGATOXIN IIIA.	5.17e+00
20	64	25.0	83	7	TX4B_AGEAP	OMEGA-AGATOXIN IVB PRE	5.17e+00
21	64	25.0		Н	BOLA_HAEIN	BOLA PROTEIN HOMOLOG.	5.17e+00
22	64	25.0		Н	AGSW_VULVU	AGOUTI SWITCH PROTEIN	5.17e+00
23	64	25.0	131	~	AGSW_MOUSE	AGOUTI SWITCH PROTEIN	5.17e+00

1 AGEW_HUMAN AGOUTI SWITCH PROTEIN 5. 1 VPE_VICSA VACOUCAR PROCESSING EN 5. 1 ECSC_BACSU PROTEIN ECSC. 1 ANGT_MOUSE TETRACYCLINE RESISTANC 7. 1 TETJ_ENTFA TETRACYCLINE RESISTANC 7. 1 TETJ_ENTFA TETRACYCLINE RESISTANC 7. 1 TEMB_HAEDU BIOPOLYMER TRANSPORT E 1. 1 UNG_CAREL UNG-6 PROTEIN PRECURSO 1. 1 UNG_CAREL UNG-6 PROTEIN PRECURSO 1. 1 UNG_CAREL UNG-6 PROTEIN PRECURSO 1. 1 UNG_LABST GLUTAMATE (NADA) RECEP 1. 1 NAEL_MOUSE GLUTAMATE (NADA) RECEP 1. 1 NASO_HUMAN MYOSIN HEAVY CHAIN, NO 1. 1 URED_KLEPN UREASE ACCESSORY PROTE 1. 1 VRD_KLEAE UREASE ACCESSORY PROTE 1. 1 TBB TRYBR TUBULIN BETA CRAIN. 1. 1 BETP_CORGL GLUTAMATE TRANSPIN 1. 1 BETP_CORGL GLUTAMATE TRANSPIN 1. 1 TBB TRYBR TUBULIN BETA CRAIN. 1. 1 BETP_CORGL GLUTAMATE TRANSPIN 1. 1 BETP_CORGL GLUTAMATE TRANSPIN 1.																						
64 25.0 132 1 AGSW HUMAN AGOUTI SWITCH PROTEIN C 25.0 397 1 CBAC_ALCSP 1-CARBOXY-3-CHLORO-3 64 25.0 493 1 VPE_VICSA VACOLOAR PROCESSING 63 24.6 477 1 ANGT MOUSE ANGIOTENSINOGEN PREC 63 24.6 639 1 TETY_ENTFA TETRACYCLINE RESISTA 62 24.2 150 1 EXBB_HAEDU BIOPOLYMER TRANSPORT 62 24.2 150 1 EXBB_HAEDU BIOPOLYMER TRANSPORT 62 24.2 1464 1 NMEI_RAT GLUTAMATE (NMDA) REC 62 24.2 1464 1 NMEI_RAT GLUTAMATE (NMDA) REC 62 24.2 1466 1 SPA2_YEAST SPA2_YEAST 160 1 URED_KIEAR GENE 34 PROTEIN 61 23.8 270 1 URED_KIEAR GENE 34 PROTEIN 61 23.8 406 1 VG34_HSVEB GENE 34 PROTEIN 61 23.8 406 1 VBB_TREAR TUBULIN BETA CCESSORY PRO 61 23.8 406 1 VBB_TREAR TUBULIN BETA CCESSORY PRO 61 23.8 406 1 VBB_TREAR TUBULIN BETA CCESSORY PRO 61 23.8 406 1 VBB_TREAR TUBULIN BETA CREATE FAIN 61 23.8 406	5.17e+00	5.17e+00	5.17e+00	7.57e+00	7.57e+00	7.57e+00	7.57e+00	7.57e+00	1.10e+01	1.10e+01	1.10e+01	1.10e+01	1.10e + 01	1.10e+01	1.60e+01	1.60e+01	1.60e+01	1.60e+01	1.60e+01	1.60e+01	1.60e + 01	1.60e+01
64 25.0 132 1 AGSW 64 25.0 397 1 CBAC 63 24.6 236 1 VPE 63 24.6 477 1 ECPG 63 24.6 639 1 TETP 63 24.6 639 1 TETP 62 24.2 150 1 EXBB 62 24.2 150 1 EXBB 62 24.2 1464 1 NWE1 62 24.2 1464 1 NWE1 62 24.2 1466 1 SPAZ 62 24.2 1466 1 SPAZ 61 23.8 270 1 URED 61 23.8 270 1 URED 61 23.8 446 1 TBB 61 23.8 446 1 TBB 61 23.8 446 1 TBB 61 23.8 446 1 TBB	SWITCH	1-CARBOXY-3-CHLORO-3,4		PROTEIN ECSC.					BIOPOLYMER TRANSPORT E	UNC-6 PROTEIN PRECURSO	[NMDA]	[NMDA]	SPA2 PROTEIN.		GENE 34 PROTEIN.			PROTEIN	BETA	PRPD PROTEIN.		DNA REPAIR PROTEIN RAD
44444444444444444444444444444444444444	AGSW_HUMAN	CBAC_ALCSP	VPE_VICSA	ECSC_BACSU	ANGT_MOUSE	TET9_ENTFA	TET1_ENTFA	TETM_STAAU	EXBB_HAEDU	UNC6_CAEEL	NME1_RAT	NME1_MOUSE	SPA2_YEAST	MY SO_HUMAN	VG34_HSVEB	URED KLEPN	URED_KLEAE	Y129_HUMAN	TBB_TRYBR	PRPD_SALTY	BETP_CORGL	RAD5 YEAST
44444444444444444444444444444444444444	Н	Н	Н	Н	Н	-	Н	-	Н	1	-1	Н	Н	Н	Н	Н	Н	 1	Н	Н	Н	-4
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	25.0	25.0	25.0	24.6	24.6	24.6	24.6	24.6	24.2	24.2	24.2	24.2	24.2	24.2	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8
40000000000000000000000000000000000000	64	64	64	63	63	63	63	63	62	62	62	62	62	62	61	61	61	61	61	61	61	61
	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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TISSUE=TESTIS;
MEDLINE: 93039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCSP OR MCS
                                                                                                                                                                                                                                                                                                                                                                                                                   LT 6
MCS_MOUSE
P15265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                  SEQUENCE
                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                              EUKARYOTA, METAZOA, NEMATODA, SECERNENTEA, RHABDITIA, RHABDITIDA, RHABDITINA, RHABDITOIDEA, RHABDITIDAE, PELODERINAE, CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
EL-SARED N.M., DONELSON J.E.;
SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE LIP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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PROTON DONG (BY SIMILARITY).
BY SIMILARITY.
POLY-GLY.
BE3B5FCE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 71; DB 1; Length 413;
Pred. No. 3.18e-01;
3; Mismatches 7; Indels
                                                                                                                                                                                                                  MATTHEWS P.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS -! - CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER
PUTATIVE ACID PHOSPHATASE C05C10.4 (EC 3.1.3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0cT-1996 (REL. 34, CREATED)
01-0cT-1996 (REL. 34, LAST SEQUENCE UPDATE)
10-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
60S RIBOSOMAL PROTEIN 110A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WORNPEP, C05C10.4; CE17370.
PROSITE; PS00666; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
PFAM; PF00328; acid_phosphat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 314 PR
381 387 BY
55 60 PO
413 AA; 46617 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPANOSOMA BRUCEI RHODESIENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 PDQCAASQNCPCTRYDLLQG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PD-CCROKTCSCRLYELLHG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z48178; E1297507;
                                                     CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN;
                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ALCOHOL +
                                                                                                                                                                                                                                                                                                                                                              JONES S.J.M.;
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P53028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                      REVISIONS
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ACT_SITE
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KLEENE K.C., SMITH J., BOZORGZADEH A., HARRIS M., HAHN L.,
KARIMDOUR I., GERSIEL J.;

Sequence and developmental expression of the mRNA encoding the
seleno-protein of the sperm mitochondrial capsule in the mouse.";
DEV. BIOL. 137:395-402(1990).

-I- FUNCTION: STRUCTURAL PROTEIN OF THE SPERM MITOCHONDRIAL CAPSULE.

IMPORTANT FOR THE MAINTENANCE AND STABILIZATION OF THE CRESCENT
STRUCTURE OF THE SPERM MITOCHONDRIAL.

-I- SUBCELLULAR LOCATION: KERATINOUS MITOCHONDRIAL CAPSULE.

-I- TISSUE SPECIFICITY: TESTIS.

-I- DEVELOPMENTAL STAGE: LATE MEIOTIC AND BARLY HAPLOID CELLS.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KARIMPOUR I., CUTLER M., SHIH D., SMITH J., KLEENE K.C.; "Sequence of the gene encoding the mitochondrial capsule selenoprotein of mouse sperm: identification of three in-phase TGA selenoprometains codone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                        Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                              8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M88463; G459886; -.
EMBL; M29603; G567228; -.
PIR; A37199; A37199.
MGD; MG196945; MCS.
MITOCHONDRION; SELENIUM; SPERM; TESTIS; SPERMATOGENESIS.
BINDING 7 SELENIUM.
                                                                                                                                                                        Score 70; DB 1; L
Pred. No. 4.80e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR'1990 (REL. 14, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69; DB 1; L. Pred. No. 7.21e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21015 MW; 4E56990C CRC32;
                                                                                                                24597 MW; EA1B6765 CRC32;
                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                   Score 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SELENIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
EMBL; U34620; G1123023; -. PROSITE; PS01199; RIBOSOMAL_L1; 1. PFAM; PF00687; Ribosomal_L1; 1. RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selenocysteine codons.";
DNA CELL BIOL. 11:693-699(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 55-197 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.0%;
llarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                52 LPHVCRPRMTVCLLCDLVH 70
                                                                                                                                                                                                                                                                                                                     3 LPDCCRQKTCSCRLYELLH 21
                                                                                                                                                                        27.3%;
                                                                                                                                                                                               Local Similarity 42.1%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 AA;
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Best Local Similarity
10; Conser
                                                                                                                      214 AA;
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"Region-specific meiotic recombination in Schizosaccharomyces pombe:
the rec11 gene.";
MOL. MICROBIOL. 23:869-878(1997).
                                                                                                                                                                                                                                                                                                                                                                     923 AA; 107418 MW; B51C7725 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (REL. 16, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.8%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.2%;
Best Local Similarity 35.7%;
Matches 10; Conservative
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38225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                   EMBL; U70737; G1619901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACETYLGALACTOSAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 90384840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALACTOSE 4 - EPIMERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S11223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 12
GALE_RAT
P18645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THIS IMMUNOCLOBULIN BELONGS TO THE IGA-G SUBCLASS. IT WAS ISOLATED FROM A RABBIT HOMOZYGOUS FOR A2, N80, DE12,15, F71, G75 HEAVY CHAIN HAPLOTYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNIGHT K.L., MARTENS C.L., STOKLOSA C.M., SCHNEIDERMAN R.D.;
"Genes encoding alpha-heavy chains of rabbit IgA: characterization of
cDNA encoding IgA-g subclass alpha-chains.";
NUCLEIC ACIDS RES. 12:1657-1670(1981 R.S. 12:1657-1670(1981 M.MUNOGLOBULIN CLASS IN BODY
SECRETIONS: IT MAY SERVE BOTH TO DEFEND ACAINST LOCAL INFECTION
AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                        01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
IG ALPHA (CHAIN C REGION (FRAGMENT).
ORYCTOLAGUS CUNICLUS (RABEIT).
ORYCTOLAGUS CUNICLUS (PABEIT).
EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA: LEFORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67; DB 1; L. Pred. No. 1.61e+00;
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MEIOTIC RECOMBINATION PROTEIN REC11.
                                                                                                                                                                                                                                                        21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
IG ALPHA CHAIN C REGION (FRAGMENT).
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SEQUENCE FROM N.A.
MEDLINE; 97231330.
LI Y.F., NUMATA M., WAHLS W.P., SMITH G.R.;
Mismatches
                                                                                                                                                                                                             299 AA
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SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                  SCSLYPVYHGSAKNNIGIKQL 235
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                                                                                13 SCRLYELLHGAGNHAAGILTL 33
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26.2%;
Best Local Similarity 50.0%;
Matches 7; Conservative
Conservative
                                                                                                                                                                                                             STANDARD;
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2 PLPDCCRQKTC-SC 14
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RE11_SCHPO
Q92380;
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P01879;
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SEQUENCE
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ID RED
AC 0.99
DT 0.01
DDT 0.01

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZESCHNIGK M., WILCKEN-BERGMANN B., STARZINSKI-POWITZ A.; "CDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli.";
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: CATALYZES TWO DISTINCT BUT ANALOGOUS REACTIONS: THE EPIMERIZATION OF UDP-GLUCOSE TO UDP-GALACTOSE AND THE EPIMERIZATION OF UDP-N-ACETYLGLUCOSAMINE TO UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: UDP-GLUCOSE = UDP-GALACTOSE.
-!- COFACTOR: NAD.
-!- PATHWAY: GALACTOSE METABOLISM.
-!- SIMILARITY: WITH OTHER GALACTOWALDENASES FROM EUKARYOTIC AND PROKARYOTIC ORIGIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 66; DB 1; Length 347; Pred. No. 2.38e+00;
Score 67; DB 1; Length 923;
Pred. No. 1.61e+00;
6; Mismatches 12; Indels
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3EC2E611 CRC32;
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                                                                                                                                  232 CCDIMRCLCLIVNKLSEKSNOTAEILVL 259
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HSSP; P09147; IKVS.
ISOMERASE; NAD; GALACTOSE METABOLISM.
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RESULT: 15

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TO STORY OF THE STANDARD; PRT; 380 AA.

TO 15-DEC-1998 (REL. 37, CREATED)

TO 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

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Search completed: Fri Aug 20 21:07:07 1999 Job time : 19 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

MasPar time 5.02 Seconds 263.383 Million cell updates/sec Fri Aug 20 21:06:09 1999; Run on:

Tabular output not generated.

Title:

>US-08-938-548B-8 (1-33) from US08938548B.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 30.710; Variance 49.199; scale 0.624 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	3.46e-03	6.20e-01	1.32e+00	1.91e+00	1.91e+00	1.91e+00	2.76e+00	3.98e+00	3.98e+00	5.71e+00	5.71e+00	5.71e+00	8.17e+00	8.17e+00	8.17e+00	8.17e+00	1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.16e+01	1.16e+01
Description	hypothetical protein	hypothetical protein	dystrophin homolog -	oct2 protein isoform	sperm mitochondrial c	hypothetical protein	tetracycline-minocycl	Ig alpha chain C regi	Ig alpha chain C regi	UDPglucose 4-epimeras	gene D3 protein - mou	transcription regulat	conserved hypothetica	keratin KAP5.5 - shee	beta-fructofuranosida	hypothetical protein	omega-agatoxin IVB -	omega-agatoxin III, 8	omega-agatoxin III, 8	omega-agatoxin IIIA -	cell division protein	pigment deposition co	agouti protein precur
ID	T00728	\$24303	A41130	860079	A37199	T01864	JN0800	AHRB	S09276	S11223	156329	B69764	C64314	146413	S33920	T01164	A44664	A54252	B54252	A42335	B64052	A46298	137143
DB	5	7	N	7	7	7	7	7	7	7	7	7	~	7	7	7	7	7	7	7	7	~	7
Length	915	147	870	93	143	533	641	299	338	347	425	479	155	197	589	806	48	26	16	9/	103	131	132
% Query Match	33.2	28.1	27.3	27.0	27.0	27.0	26.6	26.2	26.2	25.8	25.8	25.8	25.4	25.4	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0
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S24303 #type complete
hypotherical protein H19-3' - mouse
hypotherical protein H19-3' - mouse
#formal_name Mus musculus #common_name house mouse
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
10-Sep-1997
S24303
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S24303
Poirier, F.; Chan, C.T.J.; Timmons, P.M.; Robertson, E.J.;
Evans, M.J.; Rigby, P.W.J.
Development (1991) 113:1105-1114
The murine H19 gene is activated during embryonic stem cell
differentiation in vitro and at the time of implantation in

#journal #title

ACCESSIONS REFERENCE #authors

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probable iron-sulfur- cysteine proteinase (hypothetical protein Ig alpha chain C regi antho acid transport anglotensin precursor heatshock protein dna tetracycline resistan tetracycline resistan tetracycline resistan hypothetical protein hypothetical 17.9% pr laminin related prote myosin heavy chain, n N-methyl D-aspartate glutamate receptor, N SPA2 protein - yeast gene 34 protein - equ tubulin beta chain - DNA repair protein RA myosin heavy chain.	23 - Arabidopsis thal liana #common_name mo on 12-Feb-1999 #text_r, K.; Feng, J.; Kim, Y, A.; Kurz, D.; Oji aja, V.; Yu, G.; Davis, A.; Ecker, J.R. ibrary, April 1998 psis thaliana BAC F22 from GB/EMBL/DDBJ 3063438; PID:g3063461	2. Length 915; 2-03; 1. Indels 0; 3. Londer of the conservation of
B64835 S49175 H69619 S09271 B57479 A50633 A60633 A60633 A60633 A60633 A60633 A6121 JH0799 B61231 JH0799 B61231 A374 S29159 S29159 B61231 B6123	IGNMEN Comple ein F2 idopsi ence_r r, E.; M.; The EMBL D for Ar trans trans 1 SHI 3981;	Score 8 4; Mi 4; Mi https://www.nee.comple.c
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00000000000000000000000000000000000000	T00728 hypotheti #formal_n cress-19 12-Feb-19 12-Feb-19 12-Feb-19 214200 Shinn, P. Sun, H. Y.K.; H. Y. Y	tch al Similarity 8; Conse ERTCSCRAFDLLH :: :: QKTCSCRLYELLH QKTCSCRLYELLH # Forma 13-Jan 10-S
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	RESULT EWTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #authors #accessi #accessi #accessi #arce ##ref ##r	Query M Best Lo Matches Db 794 Qy 9 Qy 9 ENTRY TITLE ORGANISM

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#cross-references MUID: 90384840
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##residues 1-3
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Best Local Similarity
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ALTERNATE_NAMES
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##cross-references GB:X00353; NID:g1575; PID:g1576
IT This immunoglobulin belongs to the IgA-g subclass. It was isolated
from a rabbit homozygous for a2, n80, de12,15, f71, g75 heavy
chain haplotype.
                                                                                                                                                                                                                                                                                                                                                                                  the start codon is "TTG" encoding a "Leu" amino acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                             #authors Charpentier, E.; Gerbaud, G.; Courvalin, P.
#journal Gene (1993) 131:27-34
#title Characterization of a new class of tetracycline-resistance
gene tet(s) in Listeria monocytogenes BM4210.
#cross-references MUID:93380670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knight, K.L.; Martens, C.L.; Stoklosa, C.M.; Schneiderman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #binding_site Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp,
#status predicted
#length 641 #molecular-weight 73013 #checksum 8738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig alpha chain C region - rabbit (fragment)
#formal_name Oryctolagus cuniculus #common_name domestic
                                                                   tetracycline-minocycline resistance protein - Listeria monocytogenes (strain BM4210) plasmid pIPB11 formal name Listeria monocytogenes 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
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characterization of cDNA encoding IgA-g subclass
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#region nucleotide-binding motif A (P-loop)\
#region GTP-binding NKXD motif\
#region GTP-binding SAK/L motif\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily translation elongation factor G;
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                                                                                                                                                                                                                                                                                                                                               ##cross-references GB:L09756; NID:g406084; PID:g406085
##experimental_source strain BM4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elongation factor Tu homology
antibiotic resistance; GTP binding; P-loop
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Pred. No. 2.76e+00;
5; Mismatches 7
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                                                    #type complete
                                                                                                                                                                                                                                                                                                        ##molecule_type DNA
##residues 1-641 ##label CHA
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                                                                                                                                                                                                                                                                                                                                                                                                     the paper
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Best Local Similarity 42.9%;
Matches 9; Conservative
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plasmid
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131,220
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REFERENCE
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*superfamily immunoglobulin C region; immunoglobulin homology duplication; glycoprotein; heterotetramer; immunoglobulin; plasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. (1990) 18:5289 cDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S09276 #type fragment II alpha chain C region - rabbit (fragment) #formal_name Oryctolagus cuniculus #common_name domestic rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain immunoglobulin homology #label IGG1\
#domain immunoglobulin homology #label IGG2\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
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UDPglucose 4-epimerase (EC 5.1.3.2) - rat
UDPgalactose 4-epimerase recomment and a state sta
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16-Aug-1996
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The IgA heavy-chain gene family in rabbit: cloning and sequence analysis of 13 C-alpha genes.
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#length 338 #checksum 2169
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Pred. No. 3.98e+00;
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Best Local Similarity 50.0%;
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Similarity 50.0%;
7; Conservative
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2 PLPDCCRQKTC-SC 14
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*accession
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beta-fructofuranosidase (EC 3.2.1.26) precursor - Aspergillus
                                                                                                                                                                                                        *superfamily Methanococcus jannaschii conserved hypothetical
protein MJ0115
#length 155 #molecular-weight 17727 #checksum 834
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#title Differential expression of genes encoding a cysteine-rich keratin family in the hair cuticle.
#cross-references WUID:94358466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Boddy, L.M.; Berges, T.; Barreau, C.; Vainstein, M.H.;
Dobson, M.J.; Ballance, D.J.; Peberdy, J.F.
#journal Curr. Genet. (1993) 24:60-66
#title Purification and characterisation of an Aspergillus niger
#cross-references MUID:93365038
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keratin KAP5.5 - sheep (fragment)

#formal_name Ovis orientalis aries, Ovis ammon aries

#common_name domestic sheep

16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change

13-5ep-1998
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31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
13-Sep-1998
S33920; S36775
                                                         preliminary; nucleic acid sequence not shown; translation not shown
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##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-197 ##label JEN ##cross-references EMBL:X73435; NID:9313721; PID:9313722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 2; Length 197;
Pred. No. 8:17e+00;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                      Length 155
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#superfamily ultra-high-sulfur keratin
#length 197 #checksum 2787
                                                                                                                                                                                                                                                                                  Score 65; DB 2; Le
Pred. No. 8.17e+00;
2; Mismatches 4
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Methanococcus jannaschii. #cross-references MUID:96337999
                                                                                                                                                    TIGR:MJ0115
                                                                                                                                                                                       #map_position REV113249-112782
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Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                  Query Match 25.4%;
Best Local Similarity 53.3%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                             72 CCKITKPCPYRDYEL 86
                                                                                                                                                                                                                                                                                                                                                                                  6 CCR-QKTCSCRLYEL 19
                                                                                            ##molecule_type DNA
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                                                           ##status
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                                        #accession
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REFERENCE
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REFERENCE
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DATE
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                                                                                                                                                                      GENETICS
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1;
                                                                                                                                                                                                                         #domain signal sequence #status predicted #label SIG\
#product beta-fructofuranosidase #status experimental
#label MAT\
                                                                                                                                                                                                                                                                                                                 #binding_site carbohydrate (Asn) (covalent) #status
predicted\
#binding_site phosphate (Thr) (covalent) #status
predicted\
#predicted
#length 589 #molecular-weight 63650 #checksum 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                   #superfamily beta-fructofuranosidase glycoprotein; glycosidase; hydrolase; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                   Query Match 25.4%; Score 65; DB 2; Length 589; Best Local Similarity 42.1%; Pred. No. 8.17e+00; Matches 8; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: Fri Aug 20 21:06:31 1999 Job time: 22 secs.
##cross-references EMBL:L06844
cession S36775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           548 RLFDVLNG-GEQAIETLDL 565
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                                                                                                                                                                                                                                                                                                  254,259,318,322,
388,463,518,527
                                                                                                                                                #gene
CLASSIFICATION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                           458,475,490
                                                                           #accession
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:08:23 1999; MasPar time 1.89 Seconds 176.899 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-8 (1-33) from US08938548B.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33

Description: Perfect Score: Sequence: Title:

PAM 150 Gap 11 Scoring table:

106580 seqs, 10152877 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Database:

Mean 21.693; Variance 81.714; scale 0.265 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	4.41e+01	5.37e+01	5.37e+01	5.37e+01	7.93e + 01	7.93e + 01	9.63e+01	9.63e+01	9.63e+01	9.63e+01	9.63e+01	1.17e+02	1.17e+02	1.41e+02
	Description	Sequence 40, Applicati	40,	40,	40,	40,	40,	40,	40,	2, A	20	6, 4	9	6	11,	α,	Sequence 23, Applicati	23,		Sequence 23, Applicati	Sequence 51, Applicati	52	Sequence 10, Applicati	Sequence 2, Applicatio
	ID	PCT-US95-0	US-08-249-	US-08-734-	US-08-469-	US-08-036-	PCT-US94-0	US-08-469-	US-08-469-	PCT-US95-0	US-08-469-	US-08-485-	ns-08-290-	US-08-620-	US-08-231-	US-08-026-	US-08-137-	US-08-487-	US-08-477-	US-08-480-	US-08-233-	5223425-6	US-08-279-	us-08-658-
	DB		~	~	7	Н	m	Н	7	m	7	Н	N	г	7	Н	Н	Н	П	ч	П	4	٦	1
	Query Match Length	39	39	39	39	39	39	39	39	348	88	1167	1167	1168	1464	1464	42	42	42	42	59	222	3	283
æ	Query	25.8	25.8	25.8	25.8	25.8	25.8	25.8	25.8	25.8	25.4	25.0	25.0	25.0		24.2	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.0
	Score	99	99	99	99	99	99	99	99	99	65	64	64	64	62	62	61	61	61	61	61	9	9	29
	Result No.	1	7	m	4	Ŋ	φ	7	80	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23

59 23.0 1019 1 US-08-296- Sequence 4, Applicatio 1.41e+02 1019 2 US-08-596- Sequence 2, Applicatio 1.41e+02 1083 1 US-08-596- Sequence 2, Applicatio 1.41e+02 1083 2 US-08-596- Sequence 2, Applicatio 1.41e+02 2 US-08-757- Sequence 10, Applicatio 1.71e+02 2 US-08-757- Sequence 11, Applicatio 1.71e+02 2 US-08-757- Sequence 11, Applicatio 1.71e+02 2 US-08-757- Sequence 11, Applicatio 1.71e+02 2 US-08-757- Sequence 12, Applicatio 1.71e+02 2 US-08-757- Sequence 13, Applicatio 2.07e+02 2 US-08-757- Sequence 14, Applicatio 2.07e+02 2 US-08-757- Sequence 15, Applicatio 2.07e+02 2 US-08-757- Sequence 16, Applicatio 2.07e+02 2 US-08-757- Sequence 17, Applicatio 2.07e+02 2 US-08-757- Sequence 2, Applicatio 2.07e+02 2 US-08-758- Sequence 2, Applicatio 2.07e+02 2 US-08-758- Sequence 2, Applicatio 2.07e+02 2 US-08-758- US-08-758- Sequence 20, Applicatio 2.07e+02 2 US-08-758- US-	ALIGNMENTS T 1 PCT-US95-06046A-40 STANDARD; PRT; 39 AA. XXXXXX Sequence 40, Application PC/TUS9506846A GENERAL INFORMATION: APPLICANT: Goodarl, Andrew David; Stroobant, Paul; APPLICANT: Goodarl, Andrew David; Stroobant, Paul; APPLICANT: Chen, Maio Su! Hiles, Ian TITLE OF INVENTION: Glial Mitogenic Factors, Their TITLE OF INVENTION: Glial Mitogenic Factors, Their TITLE OF INVENTION: Preparation and Use CORRESPONDENCE ADDRESS: ADDRESSEE: Fells & Lynch CITY: New York City STREET: 805 Third Avenue CITY: New York City COMPUTER READABLE FORM: ADDRESSEE: Morderfect COMPUTER: 1BM OPERATING SYSTER: PC-DOS SOFTWER: MAN-1995 COMPUTER: The C-DOS SOFTWER: MAN-1995 FILING DATE: 25 AM-1995 FILING DATE: 25 AM-1995 FILING DATE: 25 AM-1995 FILING DATE: 32 AM-1993 FILING DATE: 33 AM-1994 FILING DATE: 33 AM-1993 FILING DATE: 33 AM-1993 FILING DATE: 33 SEP-1992 FILING DATE: 34 SEP-1992 FILING DATE: 37 SEP-1992 FILING DATE: 37 SEP-1992 FILING DATE: 37 SEP-1992 FILING DATE: 37 SEP-1992 FILING DATE: 34 SEP-1992
20000000000000000000000000000000000000	######################################

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Sequence 40, Application US/0803555B
Patent No. 5530109
GENERAL INFORMATION:
APPLICANT: Geodearl, Andrew; Stroobant, Paul;
APPLICANT: Geodearl, Andrew; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES:
ADDRESSE: Felfe & Lynch
STREET: New York City
CITY: New York City
CITY: New York
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 2; Length 39; Pred. No. 3.62e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 AA
                                                                                                                                                                                                                              NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/OCKET NUMBER: 04585/017004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/036,555B FILING DATE: 24-MAR-1993
                 US/08/469,660
                                      PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,396
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/984,085
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/951,747
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/927,337
FILING DATE: 10-AUG-1992
ATTOMARY APPLICATION NUMBER: 07/927,337
FILING DATE: 10-AUG-1992
ATTOMARY APPLICATION NUMBER: 07/927,337
ATTOMARY APPLICATION NUMBER: 07/927,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 40, Application US/08036555B
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
ICE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                              TELEFAX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.0%;
                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
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ID US-08-036-555B-40
                               FILING DATE
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Patent No. 5876973
GENERAL INFORMATION:
APPLICANT: GWYDNE, David I.; Marchionni, Mark;
APPLICANT: GWYDNE, ROBERT N.
TILLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 2; L
Pred. No. 3.62e+01;
                                                                                                                                                                                                                                                                              NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REPERENCE/DOCKET NUMBER: 04585/00200P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                   PRT;
  08/470,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40, Application US/08469660
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
CE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 428-0200 TELEFAX: (617) 428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MELLE...
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
APPLICATION NUMBER: 08/47
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
ZIP: 0211-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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GENERAL INFORMATION:
APPLICANT: JI,H, ET AL.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSE: CECCHI, STRWAY & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 2; LA
Pred. No. 3.62e+01;
1; Mismatches 1
            FILING DATE: 23-CCT-1992
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
APPLICATION NUMBER: 07/907,138
FILING DATE: 03-JUN-1992
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
APPLICATION NUMBER: 07/863,703
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INCOMMATION:
                                                                                                                                                                                       NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-7045
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9505785
   07/965,173
                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NCE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.3.
REGISTRATION NUMBER: 32:
REFERENCE/DOCKET NUMBER: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: Concurrently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.8%;
Best Local Similarity 70.0%;
   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
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PCT-US95-05785-2
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APPLICANT: Minghetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Warchionni, Mark
APPLICANT: Chen, Maio Su
APPLICANT: Hiles, Ian
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 1; Length 39;
Pred. No. 3.62e+01;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,526A
FILING DATE: 06 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 AA.
                                            APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA: 0.8. 91 07566.3
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTONEN, PAGENT INFORMATION:
NAME: TSAI, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: 10D 5250.4
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 888-9384
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/08469526A Patent No. 5792849 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40, Application US/08469526A
APPLICATION NUMBER: 07/907,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                            39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodearl, Andrew
                 30-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
               FILING DATE: 30-JUN-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.8%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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APPLICANT: Feitelson, Jerald S.
TITLE OF INVENTION: Identification of, and Uses For, Nematicidal
TITLE OF INVENTION: Bacillus thuringiensis Genes, Toxins, and Isolates
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.0%; Score 64; DB 2; Length 1167
Best Local Similarity 45.5%; Pred. No. 5.37e+01;
Matches 5; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Galnesville STRATE: Florida COUNTRY: USA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,053
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTONNEY, AGENT INFORMATION:
NAME: SALIWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/POCKET NUMBER: 31,794
REFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 1167 AA; 131657 MW; 7095219 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,717A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/540,104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08620717A Patent No. 5670365 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08620717A
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-OCT-1995
N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         873 PNCCKPAACQC 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PDCCROKTCSC 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Patent No. 5831011
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Narva, Kenneth E.
APPLICANT: Narva, Genny M.
TITLE OF INVENTION: No. 5831011el Bacillus thuringiensis Genes Encoding
TITLE OF INVENTION: No. 5831011el Bacillus thuringiensis Genes Encoding
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
C. FILING DATE: 21-MAR-1996
C. CLASSIFICATION ATA:
APPLICATION NUMBER: US/08/590,554A
C. CLASSIFICATION DATA:
C. CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/485,568
C. CLASSIFICATION DATA:
C. CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/310,197
FILING DATE: 21-SEP-1994
FILING DATE: 21-SEP-1994
FILING DATE: 21-SEP-1994
                                                                                                                                                                                                                                                                      Length 1167;
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Pred. No. 5.37e+01;
3; Mismatches 3; Indels
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein PENCE 1167 AA; 131657 MW; 7095219 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/558,738
FILING DATE: 27-JUL-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,698
FILING DATE: 16-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/918,345
FILING DATE: 21-JUL-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08590554A
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
IENGTH: 1167 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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Best Local Similarity 45.5%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   873 PNCCKPAACQC 883
                                                                                                                                                                                                                                                                                                                                                                                                               4 PDCCROKTCSC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JT 12
US-08-590-554A-6
                                                                                                                                                                                                                     SEQUENCE
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Gaps

Query Match 24.2%; Score 62; DB 1; Length 1464; Best Local Similarity 23.3%; Pred. No. 7.93e+01; Matches 7; Conservative 11; Mismatches 12; Indels 0; Gaps CC RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 to 1464 SQ SEQUENCE 1464 AA; 165489 MW; 11224000 CN;

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Search completed: Fri Aug 20 21:08:30 1999 Job time : 7 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:05:04 1999; MasPar time 5.22 Seconds 134.533 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-8

(1-33) from US08938548B.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score:

Scoring table:

Sequence:

PAM 150 Gap 11

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part8 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Variance 84.044; scale 0.274 Mean 23.069; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADTES

					SUMMARIES		
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Result	1	Query	1	6	í		
INC.	acore	MALCH.	March Length DB	80 :	ייייייייייייייייייייייייייייייייייייייי	Description	Pred. No.
1	256	100.0	123	33	W61383	Mouse HFGAN72 recepto	1.85e-18
7	. 256	100.0	130	30	W50158	Mouse hypocretin 35.	1.85e-18
m	256	100.0	130	33	W61382	Rat HFGAN72 receptor	1.85e-18
4	256	100.0	130	30	W50157	Rat hypocretin 35.	1.85e-18
Ŋ	256	100.0	131	33	W61381	Human HFGAN72 recepto	1.85e-18
φ	77	30.1	363	23	W12414	Porcine complement in	8.08e+00
7	75	29.3	373	31	W56031	Mouse ICH-3.	1.22e+01
ω	75	29.3	373	13	R66767	Murine interleukin-1	1.22e+01
თ	75	29.3	373	18	R98461	Murine ICE-ced-3 homo	1.22e+01
10	73	28.5	1876	29	W38757	Phosphatidyl inositol	1.85e+01
11	69	27.0	329	56	W29877	Lysophosphatidic acid	4.19e+01
12	99	25.8	102	-1	P95679	Xenopus Vql protein f	7.64e+01
13	99	25.8	348	51	W01619	Human uridine diphosp	7.64e+01
14	65	25.4	14	30	W52512	Cyclic peptide of the	9.31e+01
15	65	25.4	78	S	P20020	Sequence of a foot an	9.31e+01
16	65	25.4	92	30	W53894	Fragment of chimeric	9.316+01

	13e+02 13e+02	Η.	٠	Τ.	Γ.	Π.	13e+02	۲.	Π.				68e+02	٠	φ.	٥.	œ.	φ.	68e+02	.68e+02	.04e+02	.04e+02	.04e+02	2.04e+02	.04e+0	.04e+02
7-transmembra e agouti signa	signalli	cium channel inhib	nom fract	gnalli	agouti protein.	i signall	encoded by a	Ω.	Bacillus thuringiensi 1	7	ma lymphocyt	pider veno	al perip	specif	•		Glutamic acid recepto 1		ecept	receptor sub	in p	cone snail	Human membrane antige 2		Ehrlichia sp. extende 2	Human bg protein asso 2
00	W10106 R45611	R60293	R44209	010	W67568	2	W68617	W31504	W10653	W16326	W52118	R55088		W46772	R66039	W85576	R42054	R80970	552	R44192	W12745	189	733		26	94
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396	4 4 5	48	48	130	131	131	131	1167	1167	1168	583	34	142	612	46	1464	1464	4	1464	1464	42	42	S	^	439	0
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64	64 64	64	64	64	64	64	64	64	64	64	63	62	62	62	62	62	62	62	62	62	61	61	61	61	61	61
17	19 20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	38	40	41	42		44	45

ALIGNMENTS

00-007-1998 (first entry)
Mouse HFGAN72 receptor protein.
HFGAN72 receptor; eating disorders; renal disease; heart failure;
sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder. 33..65 /note= "Ligand 72A" 69..96 /note= "Ligand 72B" Location/Qualifiers standard; Protein; 123 AA EP-849361-A2.
24-JUN-1998.
24-JUN-1998.
26-SEP-1997; US-939093.
17-DEC-1996; US-033604.
19-MAR-1997; US-820519. W61383; Region W61383 Mus sp. Region

(SMIK) SMITHKLINE BEECHAM CORP.

(SMIK) SMITHKLINE BEECHAM PLC.

Bergama DJ. Brooks DP, Gellai M, Wilson S, Yanaqisawa M;

WPI; 98-324672/29.

HFGAN72 receptor ligands - and corresponding DNA, agonists,

mustice the proof of the point of the point

US-08-938-548B-8.rag

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This protein is a porcine complement inhibitor encoded by pMCPcDNA (761098). The DNA is useful for large scale production of recombinant porcine complement inhibitor, which is useful for porcine organ transplantation into humans. The DNA clone pMCPcDNA is also useful in the analysis of the promoter region of porcine complement
                                                                                                                                                                                                                                                                                                                         DNA encoding porcine complement inhibitor - useful in porcine organ
                                                                     24-SEP-1997 (first entry)

Porcine complement inhibitor.

porcine; pig; complement; inhibitor; organ transplantation; analysis; prometer.
                                                                                                                                                                                                                                                                    Murakami H, Shigehisa T, Toyomura K;
WPI; 97-087378/08.
                                    W12414 standard; Protein; 363 AA.
                                                                                                                                                                                                                                  (NIME-) NIPPON MEAT PACKERS INC.
                                                                                                                                                                                                                                                                                                                                          transplant to humans
Claim 3; Page 12-14; 20pp;
                                                                                                                                                                                      09-JAN-1997.
19-JUN-1996; J01704.
20-JUN-1995; JP-178254
                                                                                                                                                                                                                                                      (NIHA-) NIPPON HAM KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                         N-PSDB; T61098.
                                                                                                                                            Sus scrofa.
WO9700951-A1.
                                                                                                                                                                                  09-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be used for treating obesity, diabetes, anorexia nervosa, bulinia, cachexia, chronic renal failure, renal disease, congestive heart failure, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulimia and cachexia. The HFGANZ receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, Parkinson's disease, both acute and congestive heart failure, hypotension, hypotension, urinary retention, osteoporosis, angina prostatic hypertrophy, chronic renal failure, renal disease, impaired glucose tolerance, sexual dysfunction and psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or gilles dela Tourett's syndrome.
                                                                                                                                                                                                                                                                                                                                                                     Human HFGAN7 receptor protein.

Human HFGAN7 receptor: protein.

HrGAN72 receptor: eating disorders; renal disease; heart failure;

Sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;

osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;

neurological disorder.
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                                                                                                                                                                               Gaps
antagonists, in therapy, to detect Ab and to isolate cognate receptors. Oligonucleotides based on H35 cDNA can be used to detect
                               the hypocretin gene or its RNA transcript, and as antisense agents for inhibiting gene expression. H35 cDNA can also be used for recombinant protein production. The Ab can be used to detect or quantify hypocretin proteins and as a therapeutic inhibitor. Sequence 130 AA;
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                                                                                                                                          Length 130;
                                                                                                                            Score 256; DB 30; Length 130
Pred. No. 1.85e-18;
''' amatches 0; Indels
                                                                                                                                                                                                                33 qplpdccrqktcscrlyellhgagnhaagiltl 65
                                                                                                                                                                                                                                    1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33
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/note= "Ligand 72A"
70..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70..97
/note= "Ligand 72B"
                                                                                                                                                                                                                                                                                                     JT 5
W61381 standard; Protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies, antagonists, etc.
Claim 2; Fig 2; 35pp; English.
                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                        02-OCT-1998
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                                                                                                                                                                                                                                                                                                                                      W61381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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Length 363;

39.1%; Score 77; DB 23; Length 363 39.3%; Pred. No. 8.08e+00; Mismatches 9; Indels

Conservative

363 AA;

Japanese

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Transfer in the control of the control of the control of the control of a control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICH-3; mouse; programmed cell death; septic shock; folliculogenesis; interleukin converting enzyme; ICE; cysteine protease; cytokine; maturation; apoptosis; sepsis; burn; trauma; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic knock-out mice containing new Ich-3 disrupted gene
98 plqeacrrkacs-nlpdplngqvsypng 124
                                                                       (MIUR/) MIURA M.
(WANG/) WANG S.
(YUAN/) YUAN J.
Fishman JA. Miura M, Wang S, Yuan J;
WPI; 98-159183/14.
                                                                                                                                                                                                                                                                                                                                                                                           Æ
                                                                                                                                                                                                                                                                                                                                                                              W56031 standard; Protein; 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-1997; U13898.
09-AUG-1996; US-023937.
(FISH/) FISHMAN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
WO9806263-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse ICH-3
                                                                                                                                                                                                                                                                                                                                                                                                                                               W56031;
                                                                                                                                                                                                                                                                                                             THE STATE OF COLORS OF THE STATE OF COLORS OF STATE OF STATE
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Gaps

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34 qplpdccrqktcscrlyellhgagnhaagiltl 66 1. QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33

Matches

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N-PSDB; T58301
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WO9635778-A1.
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WO9803192-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a novel mammalian lysophosphatidic acid acyltransferase (LPAAT) enzyme, designated LPAAT I. Enzymes LPAAT I, LPAAT I. LPAAT I, LPAAT I, LPAAT I, LPAAT I, and LPAAT II are human homologues of non mammalian forms of LPAAT. The sequences can be used to screen for LPAAT inhibitors and to study the role of LPAAT enzymes in signal transduction and disease. note: the present sequence does not appear in the specification; it was sequence 329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1990 (first entry)
Xenopus Vg1 protein for osteogenic device.
Osteogenic device; osteogenic protein; endochronal bone; biodegradable
                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1998 (first entry)
Lysophosphatidic acid acyltransferase enzyme LPAAT I splice variant 1.
Lysophosphatidic acid acyl transferase; LPAAT; mammalian;
LPAAT inhibitor; signal transduction.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalian lyso-phosphatidic acid acyl-transferase enzymes - and related DNA, useful for isolating inhibitors and studying the role of the enzymes in signal transduction Disclosure, Page -; 5pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteogenic devices comprising matrix contg. osteogenic proteins prepd. by recombinant techniques.
Claim 7: page 48: 69pp: English.
The protein is capable of inducing endochronal bone formation in
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Pred. No. 4.19e+01;
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                                                                Indels
Pred. No. 1.85e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                        501 rrktct-rlyelisdgrtddpell 523
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                                                                                                                                                        8 ROKTCSCRLYELLHGAGNHAAGIL 31
                                                                                                                                                                                                                                                                                                                 W29877 standard; Protein; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (STAM/) STAMPS A. (YAMA-) YAMANOUCHI RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.0%;
larity 53.3%;
Conservative
                             Best Local Similarity 41.7%;
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                                                                10; Conservative
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20-7UL-1997; RD-400054.
(ELMO/) FLMNEN M A.
(FINN/) FINNEN M J.
(HILL/) HILL M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dplpgcarh-pcvcr 88
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07-APR-1989; 901469.
07-APR-1989; WO-U01469.
07-APR-1989; US-179406.
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Best Local Similarity
Matches 8; Conser
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(MAKD/) MAKDA A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 97-433268/40.
N-PSDB; T85930.
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WO8909788-A.
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association with a biocompatible, in vivo biodegradable matrix. The protein is produced by expression of the recombinant DNA in a host cell and comprises more than one polypeptide chain, with an amino acid sequence sufficiently duplicative of COP5, COP7, COP16 or OP1. The protein and the implantable devices enable optimal predictable bone formation. Clinical applications include correction of acquired and congenital cranicfacial and other skeletal or dental anomalies, induction of local endochondral bone formation in non-union fractures, peridontal applicas. requiring bone formation and cartilage repair, eg in the see also P95679-P95692 and N95097.
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W52512;
01-JUL-1998 (first entry)
Cyclic peptide of the invention.
Loop region; cyclic peptide; antimicrobial; disinfectant; therapy;
preservative; amphipathic anti-parallel beta-sheet region; plant disease.
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Claim 1; page 43-44, 59pp; Bnglish.

Human mature uridine diphosphate galactose-4-epimerase (UDP-G4E) (W01619) catalyses a reversible reaction between UDP-glucose and UDP-galactose that allows galactose residues to enter into the main UDP-galactose metabolism. A deficiency of the enzyme results in galactosaemia. The amino acid sequence of UDP-G4E was deduced from a CDNA clone (158301) derived from a human endometrial tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-APR-1997 (first entry)
Human uridine diphosphate galactose-4-epimerase.
Uridine diphosphate galactose-4-epimerase; UDP-G4E; galactosaemia;
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Pred. No. 7.64e+01;
....ma+rhes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 1; Louis Pred. No. 7.64e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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11-NAY-1995; UO5785.
11-MAY-1995; WO-UO5785.
(HUMA-) HUMAN GENOME SCI INC.
Ji H, Rosen CA;
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12 CSCRLYELLHGAGNHA 27
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12 CSCRLYELLHGAG 24
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23-JUL-1997; U12974.
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Best Local Similarity
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WPI; 96-518666/51.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp Run on:

Fri Aug 20 21:07:24 1999; MasPar time 6.81 Seconds 264.437 Million cell updates/sec Tabular output not generated.

Title:

>US-08-938-548B-8 (1-33) from USO8938548B.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILIL 33 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 30.498; Variance 47.204; scale 0.646 Statistics:

SUMMARIES

Pred. No.	-ORE 1.84e-42	1.84e-42	Н	1.84e-42	COFAC 7.54e-02	2.55e-01	3.80e-01	3-KIN 3.80e-01	3-KIN 3.80e-01	3-KIN 3.80e-01	5.64e-01	П	NT). 1.23e+00	ALP 1.23e+00	ENAS 1.82e+00	1.82e+00	AATE 2.66e+00	2.66e+00	KD P 2.66e+00	2.66e+00
Description	HYPOCRETIN (PREPRO-ORE	PREPRO-OREXIN.	PREPRO-OREXIN PRECURSO	PREPRO-OREXIN.	PORCINE MEMBRANE CO	F14B4.1 PROTEIN.	T05A1.3 PROTEIN.	PHOSPHOINOSITIDE 3	PHOSPHOINOSITIDE 3	PHOSPHOINOSITIDE 3	3' ORF.	SIMILAR TO GALACTOKINA	DYSTROPHIN (FRAGMENT)	DNA POLYMERASE III	SHIKIMATE DEHYDROGENAS	T7M24.1 PROTEIN.	INOSITOL MONOPHOSPHATE	CYCLIN G.	HYPOTHETICAL 78.2 I	TYROSINE KINASE.
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Match Length	130	130	131	131	363	752	683	1876	1876	1876	147	426	883	1135	163	533	259	293	672	1382
Query Match	100.0	100.0	100.0	100.0	30.1	28.9	28.5	28.5	28.5	28.5	28.1	27.3	27.3	27.3	27.0	27.0	26.6	26.6	26.6	26.6
Score	256	256	256	256	77	74	73	73	73	73	72	70	70	70	69	69	68	68	68	99
Result No.		7	æ	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20

3.89e+00 3.89e+00 5.66e+00 8.20e+00	8.20e+00 8.20e+00 8.20e+00 1.18e+01	1.18e+01 1.18e+01 1.18e+01	1.70e+01 1.70e+01 1.70e+01	1.70e+01 1.70e+01 1.70e+01 1.70e+01 1.70e+01	1.70e+01 1.70e+01 1.70e+01 2.44e+01
A H	ULG AND UL7 GENES, PAR BETA-D-FRUCTOFURANOSID F7N22.10 PROTEIN. COSMID CO4E6.	FROM BASES 996879 TO 1 SELENOPHOSPHATE SYNTHE SELD PROTEIN.	REPRESSOR/INDUCER PROT COSMID C27A2. RIBONUCLEASE.	T21B10.6 PROTEIN. F21C3.1 PROTEIN. AMINO ACID TRANSPORTER YUP8H12R.35 PROTEIN. TETRACYLINE RESISTANCE	ORF11. LET 852. SIMILARITY TO EGF-LIKE METALLOTHIONEIN. NONMUSCLE MYOSIN HEAVY
044954 089048 P94426 Q28584	056666 013388 065227 001473	P75863 018597 018373	005606 018238 004393	02262/ 019671 039135 064546 067709	Q57224 Q17336 Q18857 O44127 Q62706
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ALIGNMENTS

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01-NOV-1996 (TREMBLREL. 01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-OREGON
                                                                                                                      LLOYD C.;
                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Q24209
Q24209;
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                                                                                                                                                                                                                                                                                                                                                                              WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
GRAZION M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., KERSHAW J., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JOHNSTON J., PERCY C., MCMORRAN A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., FOOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VADICHAN R., WATERSTON R.,
WATERSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDMAN P.)
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIDA; RHABDITINA; RHABDITIODE; PELODERINAE; CAENORHABDITIG.
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                                                                                 Score 77; DB 6; Length 363;
Pred. No. 7.54e-02;
7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74; DB 5; Length 752; Pred. No. 2.55e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                              STEWARD C.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                              AD14F57A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84505 MW; D060D4DA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              683 AA
                                                                                                                                                                                              752 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                             98 PLQEACRRKACS-NLPDPLNGQVSYPNG 124
                                                                                                                                          2 PLPDCCRQKTCSCRLYELLHGAGNHAAG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 281078; E1346430; EMBL, 275535; E1346430; EMBL, 275535; E1346430; JOINED. EMBL, 275535; E1345510; EMBL, 261078; E1345510; OINED. PROSITE; PS00010; ASX_HYDROXYL; PROSITE; PS01209; LDLRA_1; 2. GLYCOPROTEIN; EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q22187 PRELIMINARY; PRT; Q22187; 01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                                     CREATED)
                                                                                                                                                                                               PRT;
                INT. IMMUNOL. 9:869-876(1997).
EMBL; D70897; D1021310; -.
PFAM; PF00084; sushi; 4.
                                                              363 AA; 39692 MW;
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08,
07,
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                                                                                 Query Match
Best Local Similarity 39.3%;
Matches 11; Conservative
                                                                                                                                                                              ULT 6
09473
093473
093473; 093693;
01-FEB-1997 (TREMBLREL. 05
01-NOV-1998 (TREMBLREL. 06
01-AUG-1998 (TREMBLREL. 07
F1484.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 QPLEECDTQGNCKCRL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QPLPDCCRQKTCSCRL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                         CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                          94150718
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6
                                                              SEQUENCE
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                                                   MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
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ID Q2
AC Q2
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                                                                                                                                                                                                                                                                                                                                                           WILLSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MONTIMONE B., O'CALLAGRAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATENSTON A., WEINSTOCK L., WILKINSON SPROAT J., WHILDMAN P.:
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MOLZ L.M., CHEN Y.W., HIRANO M., WILLIAMS L.T.;
"Cpk is a novel class of Drosophila Ptdins 3-kinase containing a C2
domain.";
                                                                                                CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ή,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROSOPHILA MELANOGASTER (FRUIT FLY).
EURARYOTA: METAZOA; ARTHROPODA: TRACHEATA: HEXAPODA: INSECTA;
PTERYGOTA: DIPTERA: BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73; DB 5; Lengtn vc., Pred. No. 3.80e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                             SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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Pred. No. 3.80e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1876 AA; 210504 MW; DF107ECF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 683 AA; 77437 MW; B9B00EA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1876 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHEM. 271:13892-13899(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00168; C2; 1.
PFAM; PF00454; P13.P14 kinase; 1.
PFAM; PF00613; P13Ka; 1.
PFAM; PF00787; PX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U52192; G1272420; -. FLYBASE; FBGn0015278; P13K68D.
01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-NOV-1998 (TREMBLREL. 08, PHOSPHOINOSITIDE 3-KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.5%;
50.0%;
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PFAM; PF00794; PI3K_rbd; 1
SEQUENCE 1876 AA; 21050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 268219; E1349116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans.";
NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 ECCOKKECECR-FE 394
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                   T05A1.3 PROTEIN.
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PLASMID PMT1
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MEDLINE; 92291902.
RAVIN A.J., DYER S.M., YEADON J.E., BURDEN S.J.;
"Multiple dystrophin isoforms are associated with the postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYSTROPHIN.

TORPEDO CALIFORNICA (PACIFIC BLECTRIC RAY).

EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; CHONDRICHTHYES;

ELASMOBRANCHII: RAJIFORMES: TORPEDINOIDEI: TORPEDINIDAE: TORPEDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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MEDLINE; 92064638.
TRADON J.E., LIN H., DYER S.M., BURDEN S.J.;
"Dystrophin is a component of the subsynaptic membrane.";
J. CELL BIOL. 115:1069-1076(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; DB 5; Length 426;
Pred. No. 1.23e+00;
4; Mismatches 7; Indels
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                                                                                                          SEQUENCE FROM N.A.
STRAINS-BRISTOL N2;
GATTUNG S. GOELA D., WILSON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
WATERSTON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF003739; G2105488; -.
PROSITE; PS00627; GHMP_KINASES_ATP; 1.
PROM: PF00288; GHMP_Kinases; 1.
SEQUENCE 426 AA; 47290 WW; 7CBEF743 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 ECSCRELDEICRLY-LDHGALGARLTG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane of Torpedo electric organ.'
J. PHYSIOL. (PARIS) 0:131-133(1991)
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PROSITE: PS01159; WW_DOMAIN_1; 1.
PRAM: PP00397; WW_rsp5_WWP; 1.
PFAM: PF00435; spectrin; 2.
PFAM; PF00569; 22; 1.
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01,
08,
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07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 27.3%;
Best Local Similarity 48.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 27.3%;
Local Similarity 61.5%;
hes 8; Conservative
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ID 068770 PRELIMINARY;

AC 068770,

DI 01-AUG-1998 (TREMBLREL. 07

DT 01-AUG-1998 (TREMBLREL. 07

DT 01-AUG-1998 (TREMBLREL. 07
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
DXSTROPHIN (FRAGMENT).
                                  NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               826 LLHGVGSQTSGIL 838
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| 19 LLHGAGNHAAGIL 31
elegans.";
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Q91493
Q91493;
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NEISSERIA MENINGITIDIS.
BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA
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MAIDEN M.C.J. BYGRAVES J.A., FEIL E., MORELLI G., RUSSELL J.E.,
URWIN R., ZHANG Q., ZHOU J., ZURTH K., CAUGANT D.A., FEAVERS I.M.,
ACHTMAN M., SPRATT B.G.,
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AF037797; G2745813; -.
                                                                    BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
YERSINIA.
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                                                                                                                                                                                                                                                                                                                                              Query Match 27.3%; Score 70; DB 2; Length 1135; Best Local Similarity 47.4%; Pred. No. 1.23e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 163;
                                                                                                                                                                                           , GARNES J.,
                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                            STRAIN-KIM;
HU P., ELLIOTT J., MCCREADY P., SKOWRONSKI E., GARNES
KOBAYASHI A., CARRANO A.V., BRUBAKER R., GARCIA E.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06, CREATED)
06, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                   SEQUENCE 1135 AA; 126286 MW; 4EED77D7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69; DB 2; Lv Pred. No. 1.82e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 AA
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ONA POLYMERASE III ALPHA SUBUNIT HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: Fri Aug 20 21:08:05 1999 Job time : 41 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHIKIMATE DEHYDROGENASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LPDCCRQKTCSCRL-YELLHGAGNHA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                             474 ACKLQSLMRGFGRHAAGMI 492
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imilarity 34.6%;
9; Conservative
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AC 052422
DT 01-4UN-1998 (TREMBLREL. 06
DT 01-4UN-1998 (TREMBLREL. 06
DT 01-4UG-1998 (TREMBLREL. 06
DT SHIKIMATE DEHYDROGENAEL 07
DR NEISSENIA MENIGITIDIS.
CC BACTERIA; PROTEOBACTERIA;
RN (1)
RP SEQUENCE FROM N.A.
RA ACHTMAN M.A. SPRATT B.G.;
RL SUBMITTED (DEC-1997) TO END
RR SMBL; AF037797; G2745813;
FT NON_TER 163
SQ SEQUENCE 163 AA; 17302
                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
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SEQUENCE FROM N.A.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 4.51 Seconds 132.123 Million cell updates/sec Fri Aug 20 21:09:47 1999; Run on:

Tabular output not generated.

>US-08-938-548B-9 (1-28) from US08938548B.pep 201

1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

170751 seqs, 21266608 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

a-geneseq35 Database:

:part]	2:part2 3:part3 4:part4 5:part5 6:part6 7:part7			
:part8 9:part9	10:part10	11:part11	12:part12	13:part13
4:part14	15:part15	16:part16	17:part17	18:part18
4:part19	20:part20	21:part21	22:part22	23:part23
4:part14	25:part25	26:part26	27:part27	28:part28
29:part29	30:part30	31:part31	32:part32	33:part33
34:part39	35:part35	36:part36	37:part37	38:part38
39:part39	39:part36	37:part37	38:part38	
30:part39	30:part36	37:part37	38:part38	
30:part39	30:part38	37:part38		
30:part39	30:part38	37:part38		
30:part38	37:part38	37:part38		
30:part38				

Variance 88.282; scale 0.251 Mean 22.192;

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result		% Query					
No.	Score	Match	Match Length	DB	ID	Description	Pred. No.
Н	201	100.0	123	33	W61383	Mouse HFGAN72 recepto	2.26e-11
2	201	100.0	130	33	W61382	Rat HFGAN72 receptor	2.26e-11
e	201	100.0	130	30	W50158	Mouse hypocretin 35.	2.26e-11
4	201	100.0	130	30	W50157	Rat hypogretin 35.	2.26e-11
Ŋ	190	94.5	131	33	W61381	Human HFGAN72 recepto	2.79e-10
9	99	33.8	2192	23	W21732	LexA/NuMA fusion prot	6.37e+01
7	68	33.8	2272	23	W21731	GAL4/HA/NuMA fusion p	6.37e+01
æ	99	32.8	10	4	R20235	"p33" N-terminal (2).	9.27e+01
თ	65	32.3	716	18	R99737	Retinoid X receptor i	1.12e + 02
10	65	32.3	1464		W68485	Human recombinant col	1.12e+02
11	65	32.3		24	W32881	Protein (OA-519) cros	1.12e + 02
12	64	31.8	256	σ	R45403	Deduced sequence of h	1.34e+02
13	64	31.8	256	15	R85639	MY17 preproPR-3.	1.34e+02
14	64	31.8	549	16	R92050	KM31-7 precursor.	1.34e+02
15	64	31.8	551	38	W83404	Human KM-102-derived	1.34e+02
16	64	31.8	1477	13	R67691	S. cerevisiae scaur2R	1.34e+02

Saccharomyces cerevis 1.34e+02 Ecdysone receptor lig 1.62e+02 Drosophila ecdysone rc 1.62e+02 Modified ecdysone rc 1.62e+02 Modified ecdysone rc 1.62e+02 Ecdysone receptor. 1.62e+02 DHR23alpha protein. 1.62e+02 Modified ecdysone rc 1.62e+02 Human alpha collage 1.94e+02 Human alpha-1 collage 1.94e+02 Human alpha-6(IV) col 1.94e+02 Human alpha-6(IV) col 1.33e+02 Basmid paspertide based 2.33e+02 Basmid paspertide based 2.33e+02 Basmid pasper surfac 2.33e+02 Basmid pasper surfac 2.33e+02 Basmid pasper surfac 2.33e+02 Bequence deduced from 2.33e+02 Sequence deduced from 2.33e+02 Buman 32K Asp encoded 2.33e+02 Genomic sequence of human alv 2.33e+02 Human 32K Asp encoded 2.33e+02 Human arcosR protein 2.33e+02 Human marcosR protein 2.33e+02 Human marcosR protein 2.33e+02 Human marcosR protein 2.33e+02 Human marcosR protein 2.33e+02	Hers; renal disease; heart failure; iers; renal disease; urinary retention; myocardial infarction; psychotic disorder; iers 72A" 72B" 1. Wilson S, Yanaqisawa M; corresponding DNA, agonists, ntains two ligans whose antagonists can be betes, anorexia nervosa, bulimia, cachexia sease, congestive heart failure, impaired signortion. The agonist is useful for rim and cachexia. The HFGAN7 receptor is bacterial, fungal, protozoan and viral lions caused by HVV-1 or HVV-2, pain, mia, achexia, obesity, diabetes, asthma, and congestive heart failure, and congestive heart failure, imia, cachexia, obesity, diabetes, asthma, and congestive heart failure,
W 10 4 2 4 W 10	in; 123 AA. try) protein. protein. y; cancer; Par ectoris; myoca on/Qualifiers "Ligand 72B" "Ligand 62B" "Ligand 72B" "Li
77777 77777 8777 8777 8777 8777 8777 8	try) on/o, cecto, cect
1470 5500 5500 7466 7466 1084 1084 1084 1084 1084 1084 1084 1084	ndard; Protein (first ent. N72 receptor; eatin; function; HIV (is; angina pec al disorder. Location Bosoner A2. A2. A2. A2. A2. A2. A3. A2. A2
${\tt omm}, {\tt omm}, {$	rd; (ff) (ff) (ff) (gs) (gs) (gs) (gs) (gs) (gs) (gs) (gs
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                    RESULT
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BY THIODOISES, antagonists, etc...

Claim 2: Fig 2: 35pp: English.

Claim 2: Claim 3: Claim 3:
                                                                                                                                                                                                                                                                                                                                                                                                         Human HFGAN72 receptor protein.
HFGAN72 receptor; eating disorders; renal disease; heart failure;
Exual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder.
                                                                                                                                                                                                 ö
antagonists, in therapy, to detect Ab and to isolate cognate receptors. Oligonucleotides based on H35 cDNA can be used to detect
                                                                                                                                                                                                   Gaps
                                  the hypocretin gene or its RNA transcript, and as antisense agents for inhibiting gene expression. H35 cDNA can also be used for recombinant protein production. The Ab can be used to detect or quantify hypocretin proteins and as a therapeutic inhibitor.
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                                                                                                                                                           Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HFGAN72 receptor ligands - and corresponding DNA, agonists
                                                                                                                                      Score 201; DB 30; Length Lo. Pred. No. 2.26e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP.

(SMIK ) SMITHKLINE BEECHAM PLC.

Bergsma DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M; WPI: 98-324672/29.

N-PSDB; V28138.
                                                                                                                                                                                                                                      69 rpgppglqgrlqrllqangnhaagiltm 96
                                                                                                                                                                                                                                                                             1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28
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/note= "Ligand 72A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Ligand 72B'
                                                                                                                                                                                                                                                                                                                                      ,T 5
W61381 standard; Protein; 131
                                                                                                                                                         / Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                 28; Conservative
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19-MAR-1997; US-820519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-DEC-1997; 310216
                                                                                                                  130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-849361-A2
                                                                                                                                                                                                                                                                                                                                                                             W61381;
02-0CT-1998
                                                                                                                      Seguence
                                                                                                                                                           Query Match
Best Local S
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Indiaguoses given in W21731-32 represent fusion proteins which contain The sequences given in W21731-32 represent fusion proteins which contain NuMA (nuclear mitoric apparatus). The fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30). Compounds which interfere with the interaction of NuMA with a known NIP are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIP-1; NIP-2; NuMA; nuclear mitotic apparatus; NuMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth.
                                                                                                                           LexA/NuMA fusion protein.
IPP-1; NIP-2; NuMA; nuclear mitotic apparatus; NuMA interacting protein;
cell division; proliferation; antibody; Ab; detection;
malignant cell growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding nuclear mitotic appts. interacting proteins – useful for modulating cell division and proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Residues_18-2116_of_NuMA
285..1784
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365..1864
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Pred. No. 6.37e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= LexA_DNA_binding_domain
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/label= Hemaglutinin_epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88..94
/label- Polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W21731 standard; Protein; 2272 AA.
standard; Protein; 2192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 33.8%;
Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RPGPPGLQGRLQRLLQAN 18
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01-OCT-1997 (first entry)
                                                                               01-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snyder MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1996; U09504.
07-JUN-1995; US-478408.
(UYYA.) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAL4/HA/NuMA fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McPherson SMG, Sny
WPI; 97-077270/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; T77783
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                                                                                                                                                                                                                                                                                                           Homo sapiens
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Best Local (
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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Disclosure; Fig 7; 138pp; French.

C The invention relates to the production of mammalian collagen type I gene were isolated from a MG-63 osteosarcoma library. Clone alpha3 contained sequence encoding amino acids contained sequence, whereas clone alpha2, contained sequence encoding amino acids 171-1454 of the protein and around 500 bp of the 3' untranslated region. The 2 clones were used to generate a number of fragments which were used to construct composite sequences encoding variant collagem molecules. The fragments are: (A) containing nucleotides (nt) -4 to 479;

CC The fragments are: (A) containing nucleotides (nt) -4 to 479;

CC The fragments are: (A) containing nucleotides (nt) -4 to 479;

CC The fragments are: (A) containing nucleotides (nt) -4 to 479;

CC The whole of the amino propeptide and bases (6-77 from the sequence encoding the N-terminus of the pro-collagen amino propeptide domain; (C) the whole of the amino propeptide domain (nt 72-479); (D) all of the whole of the amino propeptide domain (nt 535-1920); (E) the Draill-BamHI fragment (1709-2808) of alpha22, encoding as 567-936 of the central helicoidal domain in the ER. This sequence companies (C) the C-terminus of the C-propeptide domain; (C) the C-terminus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as prostheses for cardiac valves, ligaments or tendons; skin substitutes; gingival implants; microcapsules for perfumes; guide tubes for nerve regeneration; slow release products for antibiotics, growth factors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anticancer agents or anti-inflammatories; surgical thread and components of ointments). They are suitable for treating any disorder related to collagen dysfunction and gelatin, produced from collagen, is used to produce glues, surgical prostheses and foods.

Sequence 1464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Protein (OA-519) cross-reactive with hpr gene product.
OA-519; cross-reaction; haptoglobin related; hpr; antibody; epitope: haptoglobin 1; haptoglobin 2; cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65; DB 35; Length 1464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.12e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W32881 standard; Protein; 2509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.3%;
imilarity 64.3%;
9; Conservative
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(UYJO ) UNIV JOHNS HOPKINS.
Kuhajda FP. Pasternack GR;
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04-DEC-1990; US-622407.
26-JUL-1991; US-735522.
24-JUL-1992; US-917716.
26-JUL-1993; US-096908.
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Homo sapiens.
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17-JAN-1989;
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17-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                      egin{array}{c} egin{array}
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PR-3; preproPR-3; MY17; human neutrophil protease-3; serine protease; tumour necrosis factor alpha; Thealpha; HL60; MY17; B cell; T cell; tumour necrosis factor alpha convertase; cytokine; septic shock; rheumatoid arthritis; cachexia; cerebral malaria; graft-host disease; ischaemia/reperfusion injury; autoimmune disease; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and treating sepsis, AIDS, auto-immune disease etc.
Disclosure; Fig 2; 69pp; English.

Disclosure; Fig 2; 69pp; English.

ProTHE refers to THE having a molecular weight of about 26,000,

which is the prohormone form of ThFa. ProTHE is cleaved to a lower

molecular weight mature' form, pref. 17kb, which, in its multimeric

(usually trimeric) form, is substantially involved in producing life-
threatening physiological changes associated with sepsis. ProTHE is

cleaved by convertase. One TNF convertase is serine protease

proteinase-3, also called PR-3, P-29B or myeloblasin. A suitable

source of convertase is the HL60 call line (or extracts, or the

culture media in which it is grown). The convertase produced by

HL60 has been sequenced and is identical to the known lymphocyte

serine protease PR-3 which has other activities unrelated to TNF
                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cpds. Which inhibit formation of mature tumour necrosis factor from its precursor - identified using TNF convertase, e.g. mutein(s), antibodies or peptide phosphonate(s), for preventing and treating sepsis, AIDS, auto-immune disease etc.
Claim 2; Columns 43-60; 68pp; English.#
The present sequence is a protein (OA-519) cross-reactive with the haptoglobin related (hpr) gene product. OA-519 can be used raise antibodies reactive with epitopes found on the hpr gene product, but not on haptoglobin 1 or 2, useful in cancer, especially breast cancer, prognosis assays.
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                                                                                                                                                                                                                                                                                     Length 2509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deduced sequence of human proteinase-3 (PR-3)

TNF convertase; proteinase-3; PR-3; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CETU ) CETUS ONCOLOGY CORP.
Halenbeck RF, Jewell DA, Koths KE, Kriegler M, Perez C;
                                                                                                                                                                                                                                                        Score 65; DB 24; Length 200. Pred. No. 1.12e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.8%; Score 64; DB 9; Length 256; Best Local Similarity 38.5%; Pred. No. 1.34e+02; Matches 10; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     411 ppapaphatlprllrasgrtpeavqkl 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PGPPGLQGRLQRLLQANGNHAAGILTM 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 12
R45403 standard; Protein; 256 AA.
R45403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             т 13
R85639 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                     Query Match 32.3%;
Best Local Similarity 29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1993; U06120.
25-JUN-1992; US-905546.
                                                                                                                                                                                                                    2509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 94-026195/03.
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******	$\begin{bmatrix} \bar{1} & \bar{1} \end{bmatrix}$	*******
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:12:58 1999; MasPar time 1.89 Seconds 150.169 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-9 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

106580 segs, 10152877 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Database:

Mean 20.582; Variance 81.576; scale 0.252 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	2.72e+01	2.72e+01	2.72e+01	2.72e+01	3.30e+01	4.00e+01	4.00e+01	5.87e+01	7.10e+01	8.57e+01	8.57e+01	1.03e + 02	1.03e+02	1.03e + 02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e + 02	1.03e+02	1.03e+02
		Applicatio	Applicati	Applicatio		Applicatio	Applicatio		Applicatio	, Applicati	Applicatio	Applicati	Applicatio	Applicatio										
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence																		
	ΩI	US-08-363-	US-08-363-	US-08-363-	US-08-363-	PCT-US91-0	PCT-US95-1	US-08-469-	US-08-804-	US-08-494-	US-08-858-	US-08-858-	PCT-US93-0	US-07-949-	US-08-115-	US-08-792-	US-08-814-	US-08-017-	US-07-941-	US-07-921-	PCT-US93-0	PCT-US94-1	US-08-115-	US-07-941-
	DB	7	7	7	~	r	m	Н	7	Н	~	7	m	-	Н	Н	7	-4	Н	Н	m	m	Н	Н
	Length	442	442	445	445	10	716	2509	1841	1694	381	381	199	199	199	199	199	199	199	296	296	296	296	. 296
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	Score	29	67	67	. 67	99	65	65	63	62	61	61	09	9	9	9	9	09	09	9	09	09	9	9
	Result No.	1	7	3	4	2	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19			22	

14, Applicati 14, Applicati 14, Applicati 16, Applicati 17, Applicati 18, Applicati 19, Applicati 19, Applicati 19, Applicati 10, Applicati 10, Applicati 11, Applicati 12, Applicati 13, Applicati 14, Applicati 15, Applicati 16, Applicati 17, Applicati 18, Applicati 19, Applicati 10, Applicati 10, Applicati 11, Applicati 12, Applicati 13, Applicati 14, Applicati 15, Applicati 16, Applicati 17, Applicati 18, Applicati 19, Applicati 10, Applicati 11, Applicati 11, Applicati 12, Applicati 13, Applicati 14, Applicati 15, Applicati 16, Applicati 17, Applicati 18, Applicati 19, Applicati 10, Applicati 11, Applicati 12, Applicati 13, Applicati 13, Applicati 14, Applicati 15, Applicati 16, Applicati 17, Applicati 18, Applicati 19, Applicati 19, Applicati 10, Applicati 11, Applicati 11, Applicati 12, Applicati 13, Applicati 13, Applicati 14, Applicati 15, Applicati 16, Applicati 16, Applicati 17, Applicati 17, Applicati 18, Applicati 19, Applicati 10, Applicati 10, Applicati 10, Applicati 11, Applicati 11, Applicati 11, Applicati 12, Applicati 13, Applicati 13, Applicati 14, Applicati 15, Applicati 16, Applicati 16, Applicati 17, Applicati 17, Applicati 18, Applicati 19, Applicati 19, Applicati 10, Applicati 10, Applicati 11, Applicati 11, Applicati 11, Applicati 11, Applicati 12, Applicati 13, Applicati 14, Applicati 15, Applicati 16, Applicati 17, Applicati 17, Applicati 18, Applicati 19, Applicati 19, Applicati 10, Applicati 10, Applicati 10, Applicati 10, Applicati 10, Applicati 10, Applicati 11, Applicati 11, Applicati 11, Applicati 12, Applicati 13, Applicati 14, Applicati 15, Applicati 16, Applicati 16, Applicati 17, Applicati 17, Applicati 18, Applicati 18, Applicati 19, Applicati 19, Applicati 19, Applicati 10, Applicati 10, Applicati 10, Applicati 10, Applicati 11, Applicati 11, Applicati 11, Applicati 11, Applicati 11	
Sequence Seq	
16 1 US-08-165- 15 1 US-07-745- 15 1 US-07-745- 16 1 US-07-745- 18 2 US-08-833- 10 2 US-08-363- 11 US-07-946- 11 US-07-946- 12 US-08-363- 14 2 US-08-363- 14 2 US-08-363- 14 2 US-08-363- 14 5 10555-8 17 1 US-07-946- 18 2 US-08-363- 14 5 10555-8 17 1 US-07-946- 18 1 US-08-363- 18 1 US-08-363- 19 1 US-08-363- 10 US/08363255 11 US-07-946- 11 US-07-948- 11 US-07-08-363- 12 US-08-363- 13 US-08-363- 14 US-08-363- 14 US-08-363- 15 US-08-363- 16 US-08-363- 17 UND-RER: 25237- 18 UND-RER: 25237- 18 UND-RER: 25237- 18 UND-RER: 25237- 18 US-08-363- 18 UND-RER: 25237- 18 US-08-88- 18	0792 0: 4: CS:
293 303 303 303 303 303 303 303 303 303 3	(415) 6141 R SEC RACTE
29.99.99.99.99.99.99.99.99.99.99.99.99.9	TELEX: TELEX: 70 RMATION FO QUENCE CHA
Sequence Sequen	TELEFAX: TELEX: INFORMATION SEQUENCE C
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APPLICANT: MOOJ, WOOJI
APPLICANT: Seol, Wooji
APPLICANT: Choi, Hueng-Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/04588
FILING DATE: 19910627
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 007/544,862
FILING DATE: 27-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 3; Length 10;
Pred. No. 3.30e+01;
1; Mismatches 0; Indels
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SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16311
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                          COUNTRY: USA
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application PC/TUS9516311 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
ENCE 10 AA; 1169 MW; 376 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: 212-715-0600 TELEFAX: 212-715-0674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-715-0674
TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.8%;
88.9%;
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STATE: MA
COUNTRY: USA

CONTRY: USA
TO: 02110-2804
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                           New York
    New York
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Best Local Similarity
Matches 8; Conserv
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ID PCT-US95-16311-4
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                                                                                                                                                APPLICANT: COLLINS, DESMOND M.
APPLICANT: de LISLE, GEOFFREY W.
APPLICANT: PASCOPELLA, LISA
APPLICANT: RANKAMI, RIKU P.
TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A
TITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.3%; Score 67; DB 2; Length 445; Best Local Similarity 31.8%; Pred. No. 2.72e+01; Matches 7; Conservative 11; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                             STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
2 IP: 94304-1018
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,255
FILING DATE: 23-DEC 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application PC/TUS9104588
GENRAL INFORMATION:
APPLICANT: Browning, Jeffrey
APPLICANT: Ware, Carl F.
TITLE OF INVENTION: SURFACE COMPLEXED LYMPHOTOXIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O Fish & Neave
STREET: 875 Third Avenue, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION UNMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20002.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAS: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOGY: linear 445 AA; 48583 MW; 967304 CN;
                                                                                                         APPLICANT: JACOBS, Jr., WILLIAM R. APPLICANT: BLOOM, BARRY R.
                                      Sequence 12, Application US/08363255
Patent No. 5783386
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  E: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application PC/TUS9104588
Sequence 12, Application US/08363255
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 LQEQLHSVLDTLSEREAGVVSM 394
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LENGTH: 445 amino acids
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US-08-858-052-1
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ID US-
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DT
XX
XX
CX
XX
CC
Seq
CC
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08494168
Patent No. 5731192
GENERAL INFORMATION:
APPLICANT: Reeders, Stephen T.
APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
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  Length 1841;
                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
                                                                                                                                                                                                                                                1694 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 AA.
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Query Match 31.3%; Score 63; DB 2; L
Best Local Similarity 33.3%; Pred. No. 5.87e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40397/104/BABR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LE TYPE: protein
1694 AA; 165283 MW; 14956750 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,465
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08494168
                                                                                              1513 RDTPAALAAHLAELLATARDHGPG 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                              1694 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Wac.
COUNTRY: USA
TD. 20007-5109
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US-08-494-168-2
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Sequence 3, Application US/08858052
Patent No. 5849498
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN 3-HYDROXXISOBUTYRUL-COENZYME A
TITLE OF INVENTION: HYDROLASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
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Pred. No. 8.57e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,052
FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF-0294 US TELECOMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1575573
UENCE 381 AA; 42837 MW; 742169 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GPPGLQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                               Diskette
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity 26.9%;
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MEDIUM TYPE: Diskett
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Length 199;

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Patent No. 5437863
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or ITTLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
                                                                                                                                                    Score 60; DB 1; Length 199;
Pred. No. 1.03e+02;
3; Mismatches 0; Indels
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STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/115,680
                                                                                                                                                                                                                                                                          199 AA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDIAUSA
TELECOMMUNICATION INFORMATION:
                                          REFERENCE/DOCKET NUMBER: 5174BPCT INFORMATION FOR SEQ 1D NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 199 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE IYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                      NAME: Meinert, M. C. REGISTRATION NUMBER: 31,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 2:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 199 amino acids TYPE: amino acid
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COMPUTER READABLE FORM:
                                                                                                                                                     29.9%;
Similarity 70.0%;
7; Conservative
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ADDRESSEE: Howson ar
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COMPTOTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REFERENCE/DOCKET NUMBER: 31,602
REFERENCE/DOCKET NUMBER: 31,602
REFERENCE/DOCKET NUMBER: 3-442
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
Score 60; DB 1; Leng
Pred. No. 1.03e+02;
                                                                                                                       199 AA
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199 AA; 21429 MW; 188641 CN;
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                                                                                                                                                                                          Sequence 8, Application US/08792019B
                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                              AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
     Query Match
Best Local Similarity 70.08;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1..178
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|7 LQGRLQRLLQ 16
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7 LQGRLQRLLQ 16
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:11:47 1999; MasPar time 6.52 Seconds 234.409 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-9 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Description: Perfect Score: Sequence: Title:

PAM 150 Gap 15 Scoring table:

179066 segs, 54579741 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 30.180; Variance 51.706; scale 0.584 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	4.74e-26	4.74e-26	3.52e-25	1.15e-23	2.98e-01	4.31e-01	8.98e-01	1.85e+00	2.64e+00	3.76e+00	3.76e+00	5.34e+00	5.34e+00	5.34e+00	5.34e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	
Description	HYPOCRETIN (PREPRO-ORE	PREPRO-OREXIN.	PREPRO-OREXIN PRECURSO	PREPRO-OREXIN.	TIGHT JUNCTION PROTEIN	PAR INTERACTING PROTEI	K+ CHANNEL BETA4 SUBUN	T9J22.21 PROTEIN.	T13D8.6 PROTEIN.	LEUCINE ZIPPER WITH BA	WW DOMAIN BINDING PROT	RNA POLYMERASE SIGMA-L	HYPOTHETICAL 55.5 KD P	F22013.25.	NUMA PROTEIN.	RNA POLYMERASE SIGMA-L	YONC PROTEIN.	HYPOTHETICAL 19.6 KD P	MAXP1.	RNA POLYMERASE SIGMA F	
ID	055241	055232	077668	043612	095168	035821	P97382	048721	080740	091640	088539	085680	042651	064673	014980	085683	031955	064066	035141	P95644	
DB	11	11	φ	4	φ	11	11	10	10	13	11	~	m	10	4	7	7	σ	11	7	
% Query Match Length	130	130	131	131	1174	1277	249	145	511	331	389	162	481	1015	2115	161	178	178	413	462	
& Query Match	100.0	100.0	98.0	94.5	37.8	37.3	36.3	35.3	34.8	34.3	34.3	33.8	33.8	33.8	33.8	33.3	33.3	33.3	33.3	33.3	
Score	201	201	197	190	16	75	73	71	70	69	69	99	68	9	68	49	49	49	49	49	
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RNA POLYMERASE SIGMA F MAJOR VEGETATIVE SIGMA RNA POLYMERASE SIGMA F PNA POLYMERASE SIGMA F	POLYMERASE THETICAL 60 CULIN P60.	DNA POLYMERASE III TAU HRPG. DEOXYCYTTITINE-TEIDHOSD	UNKNOWN GENE. D-SUBUNIT OF BENZOYL-C	T24D5.1 PROTEIN. RNA-DIRECTED DNA POLYM	THYROID HORMONE INDUCE HYPOTHETICAL 41.3 KD P	CARA. H06001.2 PROTEIN.	PRISTINAMYCIN I SYNTHA TNA2, TNA1, PARTIAL AN	TRANSCRIPTIONAL ACTIVA RETINOID X RECEPTOR IN	-BINDING PROT	PUTATIVE ABC TRANSPORT FATTY ACID SYNTHASE (E
Q59913 O50539 P77951	059814 069851 027212	Q45998 Q60245	Q54224 Q57877	Q22732 Q05804	Q91654 Q09636	Q50983 O17909	Q54959 O50648	050205 060811	035851	081016 Q16702
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67 67 67	67	67	999	99	99 99	99 99	99 92	65	65	65 65
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ALIGNMENTS

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                                                                                                                                                               36.3%;
ilarity 76.9%;
Conservative
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2 PGPPGLQGRLQRL
                                SEQUENCE FROM N.A
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                                             TISSUE-BRAIN
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O80740;
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048721;
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                              SEQUENCE FROM N.A.
MEDLINE: 96421547.
BEATCH M., JESATIS L.A., GALLIN W., GOODENOUGH D.A., STEVENSON B.R.;
"The tight junction protein ZO-2 contains three PDZ
(PSD-95/Discs-Large/ZO-1) domains and an alternatively spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91084854.
WUARLN J., SCHIBLER U.;
"Expression of the liver-enriched transcriptional activator protein DBP follows a stringent circadian rhythm.";
CELL 63:1257-1266(1990).
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Pred. No. 4.31e-01;
14; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. COMIE P.A., OSSIPOW V., SCHIBLER U.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                    BEATCH M.;
SUBMITTED (AUG-1986) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (AUG-1986) TO EMBL/GENBANK/DDBJ DATA BANKS.
BEAM; PRO0595; PDZ; 3.
PFAM; PF006295; Guanylate kin; 1.
PFAM; PF00625; Guanylate kin; 1.
                                                                                                                               GOODENOUGH D.A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1277 AA; 144674 MW; 89721F79 CRC32;
                                                                                                                                                                                                                                                                                                                                                           PRT; 1277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
                                                                                                                                                                                                                                                                                            268 RSPSPELRGRPDHAGQPDSDRPIGVLLM 295
                                                                                              BIOL. CHEM. 271:25723-25726(1996)
                                                                                                                                                                                                                                                                                                                 1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       826 PGAEALHAQVERFVQQAGNQADASVAL 852
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PGPPGLQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
or suppressor protein.";
CELL BIOL. 124:949-961(1994).
                                                                                                                                                                                                                                                                                                                                                                                  05,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TREMBLREL. 03, 01-MAY-1997 (TREMBLREL. 03, 01-NOV-1998 (TREMBLREL. 08, K+ CHANNEL BETA4 SUBUNIT. MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                 Query Match 37.8%;
Best Local Similarity 32.1%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%;
Local Similarity 29.6%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL. PAR INTERACTING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U83590; G2253211;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                    region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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P97382;
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ID P9
AC P9
DT 011
DT 01
DT 01
DE K+
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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VYSOTSKAIA V.S., SCHWARTZ J.R., KWAN A., TORIUMI M., YU G., OJI, O,
LIU S., LI J., ARAUJO R., AU M., BRENDEL V., BUEHLER E., CONWAY A.B.,
CONWAY A.R., DEWAR K., FENG J., KIM C., KURTZ D., LI Y., PALM C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                  MEDLINE; 96421640.
FINK M., DUPRAT F., LESAGE F., HEURTEAUX C., ROMEY G., BARHANIN J., LAZDUNSKI M.;
"A new K+ channel beta subunit to specifically enhance Kv2.2 (CDRK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
STRAIN=CV. COLUMBIA;
STONINSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERYILLE C.R., VENTER J.C.;
SUBMITTED (ARR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC002505; G2739379; --.
SEQUENCE 145 AA; 15355 MW; 660DDF14 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73; DB 11; Leuy... -
Pred. No. 8.98e-01;
....matrhes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Best Local Similarity 39.1%; Pred. No. 1.85e+00;
Matches 9; Conservative 8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                            249 AA; 27749 MW; 8805DBE7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 AA
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                                                                                                                                                                                                                                                                                   expression.";
J. Brol. CHEM. 271:26341-26348(1996)
EMBL; U65593; G1695272; -.
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1 RPGPPGLQGRLQRLLQAN 18

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Search completed: Fri Aug 20 21:12:40 1999 Job time : 53 secs.
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RA MAEKAWA T., KURIYAMA R.;

RT MALINE; 94013066.

RA MAEKAWA T., KURIYAMA R.;

RT "Primary structure and microtubule-interacting domain of the SP-H

RT antigen: a mitotic MAP located at the spindle pole and characterized

RT antigen: a mitotic MAP located at the spindle pole and characterized

RT as a homologous protein to NuMA.";

J. CELL SCI. 105:589-600(1993).

REL SCI. 105:589-600(1993).

DR EMBL; 211583; G35119;

CONFLICT 124 124 0 -> P (IN REF. 2).

TARRITET 1587 1587 0 -> H (IN REF. 2).

TARRITET 1587 1587 0 -> H (IN REF. 2).
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NUMA PROTEIN.
HOMO SAPIENS (HUMAN).
EDKARYOTA: METAZOA: CHORDATA: VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                   01-40G-1998 (TREMBLREL. 07, CREATED)
01-40G-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-40G-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
01-40G-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
P22013.25.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA, VIRIDIPLANTAE; STRETOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE, 92176231.
YANG C.H., LAMBIE E.J., SNYDER M.;
"Numa: an unusually long colled-coll related protein in the mammalian nucleus.";
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SHINN P., BUEHLER E., DEWAR K., FENG J., KIM C., LI Y., SUN H.,
CONWAY A., CONNAY A., KURTZ D., OJI O., SHEN Y.K., TORIDMI M.,
VYSOTSKAIA V., YU G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.8%; Score 68; DB 10; Length 1015; Best Local Similarity 50.0%; Pred. No. 5.34e+00; Matches 13; Conservative 2; Mismatches 11; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 4; Length 2115;
Pred. No. 5.34e+00;
6; Mismatches 3; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AC003981; G3063463; -.
SEQUENCE 1015 AA; 111751 MW; 82FA3G3F CRC32;
   5,
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 2115 AA
                                                                                                                                        PRT; 1015 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 PTRPGLRSSLKRKRGNNGPTAATILT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL BIOL. 116:1303-1317(1992).
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
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                                 280 LQEVLQSDSNHVPSVLT 296
 Conservative
                                                       || :||:::|| :::||
|11 LQRLLQANGNHAAGILT 27
                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                     ECKER J.R.;
                                                                                                                                                        064673;
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                                                                                                                       JT 14
064673
 Matches
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:11:16 1999; MasPar time 3.39 Seconds 233.546 Million cell updates/sec Run on:

>US-08-938-548B-9 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Tabular output not generated. Title: Description: Perfect Score:

PAM 150 Gap 15 Scoring table:

Sequence:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 31.574; Variance 48.443; scale 0.652 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	6.21e-01	6.21e-01	1.33e+00	1.94e+00	1.94e+00	2.82e+00	2.82e+00	2.82e+00	4.07e+00	5.86e+00	5.86e+00	5.86e+00	5.86e+00	8.40e+00	8.40e+00	8.40e+00	8.40e+00	1.20e+01	1.20e+01	1.20e+01	1.20e+01	1.20e+01	1.20e+01
	Description	SUPEROXIDE DISMUTASE [SUPEROXIDE DISMUTASE [THYROID RECEPTOR INTER	ADRENOLEUKODYSTROPHY P	HYPOTHETICAL 96.8 KD P	NIFU PROTEIN.	RNA POLYMERASE PRINCIP	PEROXISOME BIOSYNTHESI	REGULATORY PROTEIN E2.	CUTICLE COLLAGEN 36.	COAT PROTEIN VP1.	SERINE/THREONINE PROTE	ADENYLATE CYCLASE (EC	INTERLEUKIN-11 PRECURS	MYELOBLASTIN PRECURSOR	SULFITE REDUCTASE (FER	OLIGOMYCIN RESISTANCE	HYPOTHETICAL 28 KD PRO	MITOCHONDRIAL 40S RIBO	MITOCHONDRIAL PEPTIDE	HYPOTHETICAL 63.2 KD P	PROBABLE SULFATE ADENY	HYPOTHETICAL 78.9 KD P
	ΩI	SODC_HAEPA	SODC_HAEIN	TR12_HUMAN	ALD_MOUSE	YDBH_ECOLI	NIFU_FRAAL	HRDB_STRCO	PEX1_PICPA	VE2_HPV63	CC36_CAEEL	COA1_POVLY	AFSK_STRCO	CYAA_SCHPO	IL11_MOUSE	PRN3_HUMAN	SIR_SYNP7	YOR1_YEAST	YPE1_RHORU	RT04_YEAST	RF1M_HUMAN	YEAJ_ECOLI	NODQ_RHISB	YCBY_ECOLI
	DB	Н	Н	Н	Н	Н	Н	Н	Н	Н	٦	Н	Н	Н	Н	Н	Н	Н	Н	Н	Η.	Н	+	Н
	Length	187	187	σ	736	879	79	442	1157	398	307	368	799	1692	199	256	624	1477	255	Q	4	556	633	702
æ	Query Match	35.3	35.3	34.3	33.8	33.8	33.3	33.3	33.3	32.8	32.3	32.3	32.3	32.3	31.8	31.8	31.8	31.8	31.3	31.3	31.3	31.3	31.3	31.3
	Score	7.1	71	69	68	89	49			99	65	65	65	65	64	64	64	64	63	63	63		63	63
;	Result No.	Н	7	3	4	S	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Matches

g ò ALD

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                                                                                                                                                                                                                                                                         AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
KASHIMOTO K., KIM S., KIMURA S., KITAGAWA M., KITAKAWA M., WAKINO K.,
MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,
NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., IANO M.;
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                    SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE; 97426617.
BLATTHER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
                                                                                                         GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUNCH P.K., MAT-JAN F., LEE N.A., DEAYALA B.A., CLARK SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTINOMYCETALES; FRANKINEAE; FRANKIACEAE; FRANKIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.8%; Score 68; DB 1; Len 45.8%; Pred. No. 1.94e+00; rative 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I -> L (IN REF. 3
8BFD7CF3 CRC32;
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32, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
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HARRIOTT O.T., HOSTED T.J., BENSON D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RUDD K.E.;
UNPUBLISHED OBSERVATIONS (MAR-1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000235; G1787646; -.
EMBL; D90776; G1742260; -.
EMBL; D90777; G1742264; -.
EMBL; D36928; -; NOT_ANNOTATED_CDS.
ECCGENE; EG13180; YDBH.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 GVDGRLQAILQAHENELGDFVLHM 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GLQGRLQRLLQANGNHAAG-ILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  879 AA; 96834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-331 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (REL.
01-NOV-1995 (REL.
01-OCT-1996 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIFU PROTEIN
  ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRANKIA ALNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIFU_FRAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CPI1
                                                                                                                                                                                                                                                             STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RUDD K.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PROBABLE).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS). BELONGS TO THE MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adrenoleukodystrophy gene.";
MAMM. GENOME 5:810-813(1994).
-!- FUNCTION: PROBABLE TRANSPORTER. COULD BE INVOLVED IN THE
IMPORT OF VLCFA-COA SYNTHETASE INTO THE PEROXISOMAL MEMBRANE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:99672; ALDGH.
PROSITE: PSOOGII; ABC_TRANSPORTER; 1.
PFAM; PFOONO5; ABC_TRAI; 1.
ATP-BINDING; GLYCOPROTEIN; TRANSMEMBRANE; TRANSPORT; PEROXISOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SARDE C.O., THOMAS J., SADOULET H., GARNIER J.M., MANDEL J.L.; "CDNA sequence of Aldgh, the mouse homolog of the X-linked
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P52645; P77502; P76855; (1-02T-1996 (REL. 34, CREATED) (1-00T-1997 (REL. 35, LAST SEQUENCE UPDATE) (1-00T-1997 (REL. 35, LAST ANNOTATION UPDATE) HYPOTHETICAL 96.8 KD PROTEIN IN LDHA-TYNA INTERGENIC REGION.
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches 10; Indels
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D373B00E CRC32;
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                                                                                                                                                                        P48410;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ADRENOLEUKODYSTROPHY PROTEIN HOMOLOG (ALDP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
4; Mismatches
                                                                                                                                                         736 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     704 AGIPKMOGRLQELRQILGEAAAPVQPL 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| | :||||| | | |: || : : : PGPPGLQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.8%;
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81858
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z33637; G520955; -.
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                                                                                                                                                         STANDARD;
                                    289 KPGPSGLQAKLASL 302
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353
493
                                                          :|||:|||:|| | 1
1 RPGPPGLQGRLQRL 14
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TISSUE=FIBROTIC LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333
473
507
736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 95201443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESCHERICHIA COLI
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YDBH_ECOLI
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TRANSMEM
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SEQUENCE
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          noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAWLITA M., CLAD A., ZUR HAUSEN H.;
"Complete DNA sequence of lymphotropic papovavirus: prototype of a
mea species of the polyomavirus genus.";
NIROLOGY 143:196-211(1965).
-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 72 ICOSAHEDRAL UNITS,
EACH OF WHICH IS COMPOSED OF FIVE COPIES OF VP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; POLYOMAVIRUS.
                                                                                                                                                                                             FAMILY; COLLAGEN
             entities 1. entities 1. entities 1. entities 2. entites 2.
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 1; Length 368; Pred. No. 5.86e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; Louis Pred. No. 5.86e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4979282C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (REL. 33, LAST SEGUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
03-T PROTEIN VP1.
LYMPHOTROPIC POLYOMAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     799 AA.
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  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 32.3%; Score 65; Local Similarity 32.0%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 KPGNQGLDPKAKPLLDKDGNYPVEV 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00718; Polyoma_coat; 1. HSSP; P49302; 1SIE. LATE PROTEIN; COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 AA; 40211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            32.3%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 PGPPGPAGQPGRVIQVNG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PGPPGLQGRLQRLLQANG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; K02562; G333278; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 86045879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1986 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A03627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COA1_POVLY
P04010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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DT 01
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                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNNGGT-3') PRESENT
IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
PAULEY A.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
-!- SUBMNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification, sequence and expression patterns of the Caenorhabditis elegans col-36 and col-40 collagen-encoding genes."; GENE 137:281-285(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLY PROTEIN: TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; TRANS-ACTING FACTOR; DNA REPLICATION; REPRESSOR; NUCLEAR PROTEIN SEQUENCE 398 AA; 45450 MW; C9BBOCEO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 398,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 1; L
Pred. No. 4.07e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CUTICLE COLLAGEN 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 AA
                                                                                                                                                                                                                                             SUBUNIT: BINDS DNA AS A DIMER.
                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 56.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X70828; G312096; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 RSPPKGGQSRLRRLIQ 310
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1 RPGPPGLQGRLQRLLQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00508; E2_N; 1.
PF00511; E2_C; 1.
P17383; 1DHM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE; 94131298.
LEVY A.D., KRAMER J.M.;
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                                                                                                                                                                                          REPLICATION.
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coning of cDNA for proteinase 3: a serine protease, antibiotic, and coantigen from human neutrophils."; EXP. MED. 172:1709-1715(1990).
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WILDE C.G., SNABLE J.L., GRIFFITH J.E., SCOTT R.W.;
"Characterization of two azurphil granule proteases with active-site homology to neutrophil elastase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BORIES D., RAYNAL M.-C., SOLOMON D.H., DARZYNKIEWICZ Z., CAYRE Y.E., "Down-regulation of a serine protease, myeloblastin, causes growth
BURKHART-SCHULTZ K.J., GORDON L., KYLE A., RAMIREZ M., STILWAGEN S., PHAN H., VELASCO N., DO L., REGALA W., TERRY A., GARNES J., DANGAMAN L., POUNDSTONE P., CRRISTENSEN M., GEORGESCU A., AVILA J., LUU S., ATTIX C., ANDRRISE T., TRANKHEIM M., AMICO-KELLER G., COEFTELD J., DUARTE S., LUCAS S., BRUCE R., THOMAS P., QUAN G., KRONMILLER B., ARELLANO A., MONTGOMERY M., OW D., NOLAN M., TRONG S. SUBMITLER B., OLSEN A.S., CARRANO A.V.; SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                CAMPANELLI D., MELCHIOR M., FU Y., NAKATA M., SHUMAN H., NATHAN C., GABAY J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arrest and differentiation of promyelocytic leukemia cells."; CELL 59:959-968(1989).
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ZIMMER M., MEDCALF R.L., FINK T.M., MATTWANN C., LICHTER
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SEQUENCE OF 28-47 AND 196-219.
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-APR-1990 (REL. 14, CREATED)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37,
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"MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;
"Molecular cloning and characterization of murine interleukin-11.";
EXP. HEMATOL 24.1359-1376(1996).

1- FUNCTION: THIS PROTEIN STIMULATES PLASMACYTOWA PROLIFERATION,
T-CELL-DEPENDENT DEVELOPMENT OF IMMUNOGLOBULIN-PRODUCING B
CELLS AND SYMERGIZES WITH IL-3 IN SUPPORTING WURINE
MEGAKARYCOTTE COLONY FORMATION (BY SIMILARITY).
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MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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LAMERDIN J.E., MCCREADY P.M., SKOWRONSKI E., ADAMSON A.W.,
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LABBAYE C., MUSETTE P., CAVRE Y.E.;
"Wegener autoantigen and myeloblastin are encoder PROC. NATL. ACAD. SCI. U.S.A. 88:9253-9256(1991)
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21522 MW; 1CB30772 CRC32;
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
INTERLEUKIN-11 PRECURSOR (IL-11).
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MGD; MGI:107613; IL11.
CXTOKINE; GROWTH FACTOR; SIGNAL.
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199 AA;
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170751 seqs, 21266608 residues Searched:

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scale 0.251 Variance 88.282; Mean 22.192; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Mouse HFGAN72 recepto	Rat HFGAN72 receptor	Mouse hypocretin 35.	Rat hypocretin 35.	Human HFGAN72 recepto	LexA/NuMA fusion prot	GAL4/HA/NuMA fusion p	"p33" N-terminal (2).	Retinoid X receptor i	Human recombinant col	Protein (OA-519) cros	Deduced sequence of h	MY17 preproPR-3.	KM31-7 precursor.	Human KM-102-derived	S. cerevisiae scaur2R
SUMMARIES	ΙΒ	W61383	W61382	W50158	W50157	W61381	W21732	W21731	R20235	R99737	W68485	W32881	R45403	R85639	R92050	W83404	R67691
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Saccharomyces cerevis 1.34e+02 Ecdysone receptor 1ig 1.62e+02 Drosophila ecdysone r 1.62e+02 Modified ecdysone rec 1.62e+02 Modified ecdysone rec 1.62e+02 Ecdysone receptor. DHR23alpha protein. 1.62e+02 DHR23alpha protein. 1.62e+02 Modified ecdysone rec 1.62e+02 Tylactone synthase OR 1.62e+02 Tylactone synthase OR 1.62e+02 Tylactone synthase OR 1.62e+02 Human alpha-1 collage 1.94e+02 Human alpha-6(IV) col 1.94e+02 Human alpha-6(IV) col 1.94e+02 Human alveolar surfac 2.33e+02 Sequence deduced from 2.33e+02 Sequence deduced from 2.33e+02 Sequence deduced from 2.33e+02 Sequence deduced from 2.33e+02 Sequence of human alv 2.33e+02 Genomic sequence of h 2.33e+02 Human 32K ASP encoded 2.33e+02 Human marcoSR protein 2.33e+02	NTS ; renal disease; heart failure; arkinson's disease; urinary retention; cardial infarction; psychotic disorder; s	ilson S, Yanagisawa M; Tesponding DNA, agonists, Tresponding DNA, agonists, The agonist is neckeria, The agonist is useful for The agonist is obegin The HTGAN? The agonist is a seful for The agonist is obegin The HTGAN? To THY-2, pain, The agonist is diabetes, asthma, The congestive heart failure, The agonist is angina
M10424 W45513 W33655 W33656 W33656 W33656 W33656 W3656 W3656 W3656 W3656 W66237 W66441 P70662 P66665 P66665 P66665 W64217 W64217 W64217 W64217 W64217 W64217	ALIGNMENT 123 AA.) otein. disorders; cancer; Par oris; myoca	PP-849361-A2. YEP-849361-A2. 24-JUN-1998. 17-DEC-1997; 310216. 26-SEP-1997; 05-939093. R 17-DEC-1996; US-938093. R 17-DEC-1996; US-820519. R 2-JUL-1997; US-820519. R 2-JUL-1997; US-887382. R 2-JUL-1997; US-820519. R MAR-1997; US-820519. R 19-MAR-1997; US-820519. R 2-JUL-1997; US-820519. R SMIK) SMITHKINE BEECHAM CORP. THEGAN'2 receptor Jigands - and correspon antibodies, antagonists, etc. THEGAN'2 receptor ligands - and correspon antibodies, antagonists, etc. The HEGAN'2 receptor protein contains two used for treating obesity, diabetes, ano chronic renal failure, renal disease, conquesse tolerance and sexual disease, concurrently anorexia nervosa, bulimia and congruences, anorexia nervosa, bulimia and concurs, anorexia nervosa, bulimia, cach Parkinson's disease, both acute and congruences. R PROFENSION, hypertension, urinary retension, pretension, ulcers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The HFGAN72 receptor protein contains two ligands whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bulimia, cachexia, chronic renal fallure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulimia and cachexia. The HFGAN72 receptor ligand is useful for treating e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, Parkinson's disease, both acute and congestive heart failure, hypotension, hypotension, unimary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign prostatic hypertrophy, chronic renal failure, renal disease, impaired allucose tolerance, sexual dysfunction and psychotic and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human HFGAN72 receptor protein.
HFGAN72 receptor; eating disorders; renal disease; heart failure;
HFGAN72 receptor; eating disorders; renal disease; heart failure;
exual dysfunction; HIV; cancer; Parkinson's disease; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
neurological disorder.
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                                                                                                                                                                                                                                                         Gaps
antagonists, in therapy, to detect Ab and to isolate cognate receptors. Oligonucleotides based on H35 cDNA can be used to detect
                                              the hypocretin gene or its RNA transcript, and as antisense agents for inhibiting gene expression. H35 cDNA can also be used for recombinant protein production. The Ab can be used to detect or quantify hypocretin proteins and as a therapeutic inhibitor. Sequence 130 AA;
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Pred. No. 2.79e-10;
2; Mismatches 0; Indels
                                                                                                                                                                                                          Length 130;
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                                                                                                                                                                             Score 201; DB 30; Length 13.
Pred. No. 2.26e-11;
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(SMIK ) SMITHKLINE BEECHAM PLC.

Bergsma DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M; WPI: 98-124672/29.

N-PSDB; V28138.
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/note= "Ligand 72B"
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hes 26; Conservative
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17-DEC-1996; US-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
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17-DEC-1997; 310216
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                                                                                                                                              NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NuMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth.
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Pred. No. 6.37e+01;
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/label= Residues_18-2116_of_NuMA
365..1864
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/label= GAL4_DNA_binding_domain
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T 6
W21732 standard; Protein; 2192
W21732;
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GAL4/HA/NuMA fusion protein.
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                                                                                                                                    LexA/NuMA fusion protein.
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07-JUN-1995; US-4784
(UXYA ) UNIV YALE.
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WPI, 97-077270/07.
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Construct composite sequences encoding variant collagen molecules.

The 2 clones were used to generate a number of fragments which were used to construct composite sequences encoding variant collagen molecules.

The fragments are: (A) containing nucleotides (nt) -4 to 479;

Co (pathogenesis-related protein ) Signal peptide and bases 66.77 from the sequence encoding the N-terminus of the pro-collagen amino propeptide domain; (C) the whole of the amino propeptide domain (nt 72-479); (D) all containing TAA upstream of the pro-collagen amino propeptide domain; (C) the whole of the amino propeptide domain (nt 72-479); (D) all containing the N-terminus of the DrazIII-BamHI fragment

Co f the amino-telopeptide domain (nt 474-534) and the N-terminus of the helicoidal region (nt 53-1920); (E) the DraIII-BamHI fragment

Co f the BamHI-ECORI (2803-4362) region of alpha22, encoding as 396-1192 in the central helicoidal domain and as 1193-144 in the containing the C-terminus of the C-propeptide domain; (C) the C-terminus of the C-propeptide domain; (G) the contrained of the contrained
Disclosure; Fig 7; 138pp; French.
The invention relates to the production of mammalian collagen in plants.
2 clones: alpha3 and alpha22, spanning the human collagen type I gene were isolated from a MG-63 costeosarcoma library. Clone alpha3 contained 83 bp of the 5' untranslated region and the first 1920 bp of coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 35; Length 1464;
Pred. No. 1.12e+02;
1; Mismatches 4; Indels 0
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24-JAN-1989; US-188426.
17-JAN-1989; US-297722.
04-DEC-1990; US-297722.
26-JUL-1991; US-735522.
24-JUL-1992; US-917716.
26-JUL-1999; US-906908.
05-JUN-1995; US-906908.
(UVJO) UNIV JOHNS HOPKINS.
KUMJÖM FP, Pasternack GR; WPI: 97-469916/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.3%;
Best Local Similarity 64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prognosis assay.
Homo sapiens.
US565874-A.
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Trong its precursor - identified using TNF convertase, e.g.

from its precursor - identified using TNF convertase, e.g.

Trom its precursor - identified using TNF convertase, e.g.

Trom its precursor - identified using TNF convertase, e.g.

Trom its precursor - identified phosphonate(s), for preventing

Trom treating sepsis, AIDS, auto-immune disease etc.

Disclosure; Fig 2; 69pp; English.

ProTNF refers to TNF having a molecular weight of about 26,000,

Which is the prohomone form of TNFa. ProTNF is cleaved to a lower

Consully trimeric) form, is substantially involved in producing life-

threatening physiological changes associated with sepsis. ProTNF is

cleaved by convertase. One TNF convertase is serine protease

proteinase-3, also called PR-3, P-29B or myeloblasin. A suitable

source of convertase is the HL60 cell line (or extracts, or the

culture media in which it is grown). The convertase produced by

Culture media in which it is grown). The convertase produced by

Serine protease PR-3 which has other activities unrelated to TNF
                                                                                                                                                                                                                                                                                                                                                               ö
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MX17 preproPR-3.
MX17 preproPR-3.
MX17; human neutrophil protease-3; serine protease;
tumour necrosis factor alpha; TNFalpha; HLG0; MX17; B cell; T cell;
tumour necrosis factor alpha convertase; cytokine; septic shock;
rheumatoid arthritis; cachexia; cerebral malaria; graft-host disease;
ischammia/reperfusion injury; autoimmune disease; AIDS.
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                      2
Claim 2; Columns 43-60; 68pp; English.#
The present sequence is a protein (OA-519) cross-reactive with the haptoglobin related (hpr) gene product. OA-519 can be used raise antibodies reactive with epitopes found on the hpr gene product, but not on haptoglobin 1 or 2, useful in cancer, sepecially breast cancer, prognosis assays.
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                                                                                                                                                                                                                                                                                           Length 2509;
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                                                                                                                                                                                                                                                                                       Score 65; DB 24; Length 250 Pred. No. 1.12e+02; 10; Mismatches 9; Indels
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Halenbeck RF, Jewell DA, Koths KE, Kriegler M, Perez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.8%; Score 64; DB 9; Length 256; larity 38.5%; Pred. No. 1.34e+02; Conservative 7; Mismatches 9; Indels
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Deduced sequence of human proteinase-3 (PR-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                   411 ppapaphatlprllrasgrtpeavgkl 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGPPGLQGRLQRLLQANGNHAAGILTM 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 rppspalasvllalllsgaaraaeiv 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R85639 standard; Protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 256 AA
                                                                                                                                                                                                                                                                                       Query Match 32.3%;
Best Local Similarity 29.6%;
Matches 8; Conservative
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25-JUN-1992; US-905546.
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WPI; 94-026195/03.
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WO9400555-A.
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(EE)	***************************************

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:24:10 1999; MasPar time 1.85 Seconds 153.946 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-12 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

106580 seqs, 10152877 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Database:

Mean 20.582; Variance 81.576; scale 0.252 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.72e+01	2.72e+01	2.72e+01	2.72e+01	3.30e+01	4.00e+01	4.00e+01	5.87e+01	7.10e+01	8.57e+01	8.57e+01	1.03e+02	1.03e + 02	1.03e+02	1.03e + 02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e+02	1.03e + 02	1.03e+02	1.03e+02
	Applicatio	, Applicati	Applicatio	, Applicati	Applicatio	Applicatio	, Applicati	Applicatio	, Applicati	Applicatio	, Applicati	Applicatio	Applicatio										
Description	Sequence 4,	Sequence 11	Sequence 5,	Sequence 12	Sequence 3,	Sequence 4,	Sequence 10	Sequence 6,	Sequence 2,	Sequence 3,	Sequence 1,	Sequence 2,	Sequence 4,	Sequence 2,	Sequence 8,	Seguence 4,	Sequence 4,	Sequence 2,	Sequence 14	Sequence 4,	Sequence 14	Sequence 4,	Sequence 4,
ΩI	US-08-363-	US-08-363-	US-08-363-	US-08-363-	PCT-US91-0	PCT-US95-1	US-08-469-	US-08-804-	US-08-494-	US-08-858-	US-08-858-	PCT-US93-0	US-07-949-	US-08-115-	US-08-792-	US-08-814-	US-08-017-	US-07-941-	US-07-921-	PCT-US93-0	PCT-US94-1	US-08-115-	US-07-941-
DB	~	7	~	~	m	m	Н	~	Н	~	~	m	Н	Н	Н	~	Н	Н	Н	m	ო	Н	П
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% Query Match	33.3	33.3	33.3	33.3	32.8	32.3	32.3	٠.	30.8	30.3			29.9	٠,	29.9		29.9	٠.		٠.	29.9	29.9	29.9
Score	29	67	29	67	99	65	65	63	62	19	19	09	9	9	09	9	9	9	9	9	09	09	09
Result No.	1	7	3	7	5	9	7	α,	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.03e+02 1.03e+02 1.03e+02 1.03e+02 1.03e+02 1.03e+02 1.03e+02 1.03e+02 1.03e+02 1.25e+02 1.2					
Sequence 14, Applicati Sequence 14, Applicati Sequence 14, Applicati Sequence 14, Applicati Sequence 10, Applicati Sequence 10, Applicati Sequence 3, Applicatio Sequence 2, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio Sequence 6, Applicatio Sequence 16, Applicatio Sequence 16, Applicatio Sequence 16, Applicatio Sequence 16, Applicatio Sequence 16, Applicatio Sequence 16, Applicatio Sequence 10, Applicatio Patent No. 5215895. Patent No. 517525.		442 AA.		VIRULENCE FACTORS AND A FOR THEIR IDENTIFICATION 0, Version #1.30 255	
US-08-165- US-07-745- US-08-794- US-08-363- US-08-363- US-08-363- US-08-363- US-08-363- US-08-363- US-08-363- US-08-363- US-08-363- US-08-659-	ALIGNMENTS	RD; PRT;	/08363255	M. M. M. SY W. SY ERION S. SY ERION S. S. SY ERION S. S. SY ERION S. S. SY ERION S. S. SY	
, 296 4 000 5 206 6 10 6 20 6 20 6 20 6 20 6 20 6 20 6 20 6 2		STANDARD;	Application US/0836	Sequence 4, Application US/0836: Patent No. 578386 GENERAL INFORMATION: APPLICANT: JACOBS, Jr., WILL APPLICANT: GLINS, DESMOND APPLICANT: ACLINS, DESMOND APPLICANT: PASCOPELLA, LISA APPLICANT: RAWARAMI, RIKU P. TITLE OF INVENTION: MYCOBACT TITLE OF INVENTION: MYCOBACT TITLE OF INVENTION: MYCUBACT TITLE OF INVENTION: TO STATE: CONFUSES: ADDRESSE: ADDRESSEE: MORRISON & FOEIS STATE: California COUNTRY: USA ZIP: 94304-1018 COMPUTER READBLE FORM: MEDIUM TYPE: FLORPY disk COMPUTER: IBM PC COMPATION OPPRATION SYSTEM: PC-1994 CLASSIFICATION NUMBER: US/08; FILING DATE: Z3-DEC-1994 CLASSIFICATION NUMBER: Z3-43 REFERENCE/DOCKET NUMBER: Z1-43 REFERENCE/DOCKET NUMBER: Z1-43 REFERENCE/DOCKET NUMBER: Z1-43 TELEFAX: (415) 813-5600	
0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.		3-255-4	4, Appli	quence 4, Application tent No. 578386 ENERAL INFORMATION: APPLICANT: JACOBS, APPLICANT: BLOOM, BAPPLICANT: BECOM, BAPPLICANT: GELISLE APPLICANT: GELISLE APPLICANT: AMAKAMI TITLE OF INVENTION: TOWNER OF SEQUENCES: CORRESPONDENCE ADDRESSEE: ADDRESSEE: MORRIS STREET: 755 PAGE COMPUTER: IBM PC OMPUTER: IBM PC OMPUTER	
22 22 22 22 22 22 22 22 22 22 22 22 22	F.	SULT 1 US-08-363 XXXXXX	Sequence	Sequence 4, Patent No. 5 GENERAL INF APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT TITLE OF TITLE	
(44444444444444444444444444444444444444	0 0	KESUI ID XX AC	X D X D X	*8888888888888888888888888888888888888	

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TELEFAX: 202-639-7700
TELEFAX: 202-639-7890
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                        SS: single
linear
                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                           Query Match 32.3%;
Best Local Similarity 29.6%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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US-08-804-227C-6
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                                     TELEX
                                                                                                                                                                      SEQUENCE
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Pred. No. 4.00e+01;
7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                    2509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08469005A
Patent No. 5665874
GENERAL INFORMATION:
APPLICANT: RUHAJDA, FRANCIS P.
APPLICANT: PASTERNACK, GARY A.
TILLE OF INVENTION: CANCER RELATED ANTIGEN NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
                 APPLICATION NUMBER: 08/372,652
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/246001
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
TELEFAX: 617/542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 716 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTE: IBM Compatible
COMPUTE: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,005A
FILING DATE: 05-UNN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/188,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 062482-0113
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                    MOLECULE TYPE: DNA
JENCE 716 AA; 80130 MW; 2569266 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 08/096,908
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 07/917,716
FILING DATE: 24-JUL-1992
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08469005A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COUNTRY: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Posorske, Laurence H
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                single
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                                                                                                                                                                                                                                     Match 32.3%;
Local Similarity 38.9%;
les 7; Conservative
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                                                                                                                                                                       TYPE: STRANDEDNESS: SIE
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                                                                                                                                                                                           TOPOLOGY:
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Gaps
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Pred. No. 4.00e+01;
10; Mismatches 9; Indels
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Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Ribitoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NOMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1841 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
                                                                                                                                                                                   ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
JENCE 2509 AA; 273089 MW; 32011381 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
JENCE 1841 AA; 191190 MW; 14819276 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                    411 PPAPAPHATLPRLLRASGRTPEAVOKL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08804227C
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PGPPGLQGRLQRLCQANGNHAAGILITM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X -
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 317-276-2459 INFORMATION FOR SEQ ID NO: 6:
                                                LENGIH: 2509 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1841 amino acids
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Sequence 3, Application US/08858052
Patent No. 5849498
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Gueglar, Karl J.
APPLICANT: Corley, Nell C.
TITLE OF INVENTION: HUMAN 3-HYDROXYISOBUTYRUL-COENZYME A
TITLE OF INVENTION: HYDROLASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                               Sequence 3, Application US/08858052
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                 Palo Alto
                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                STREET: 317.
CITY: Palo STATE: CA
COUNTRY: US.
ZIP: 94304
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                                Gaps
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                                                                                                                                                                                                                                                                                                    APPLICANT: Reeders, Stephen T.
APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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Pred. No. 7.10e+01;
0; Mismatches 1; Indels
  Length 1841;
                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 AA.
 Score 63; DB 2; L. Pred. No. 5.87e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 40397/104/BABR TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300 TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                               8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
IENCE 1694 AA; 165283 MW; 14956750 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,465
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                           Sequence 2, Application US/08494168
Patent No. 5731192
GENERAL INFORMATION:
                                                                                                                                                                                                                                  Sequence 2, Application US/08494168
                                                        1513 RDTPAALAAHLAELLATARDHGPG 1536
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1694 amino acids
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Query Match 31.3%;
Best Local Similarity 33.3%;
Matches 8; Conservative
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Best Local Similarity 88.9%;
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US-08-858-052-3
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ID US-
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PF-0294 US

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                                                                                                                              Length 381;
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Pred. No. 8.57e+01;
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                                                                               LIBRARY: GenBank
CLONE: 1575573
ICE 381 AA; 42837 MW; 742169 CN;
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                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08858052
Patent No. 5849498
                                                                                                                                                                           298 SPTSLKITLRQLMEGSSKTLQEVLTM 323
                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08858052
                                                                                                                                                                                                  3 GPPGLQGRLQRLLQANGNHAAGILTM 28
                        : 381 amino acids
amino acid
                                                                                                                                                                                                                                                 STANDARD;
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                               single
                                                                                                                             Match 30.3%;
Local Similarity 26.9%;
Les 7; Conservative
                                                            linear
                                                                     IMMEDIATE SOURCE
                                             STRANDEDNESS:
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Patent No. 5437863
CENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
CORRESPONDENCE ADDRESS:
ADDRESSEET: Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 AA.
                                                                                                                                                                                                                                                                                                                                                     / Match 29.9%; Score 60; DB 1; L. Local Similarity 70.0%; Pred. No. 1.03e+02; les 7; Conservative 3; Mismatches 0
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: 5174BPCT
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFENCE/DOCKET NUMBER: INDIAUSA
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEPHONE: (215) 540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 199 amino acids
TYPE: amino acid
TYPE: linear
TOPOLOGY: linear
MOLEGCIE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFFCATION: 314
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31.602
REGISTRATION NUMBER: 31.602
REGISTRATION NUMBER: A-442
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
**NWCTH: 199 amino acids
     Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60; DB 1; Length 199;
Pred. No. 1.03e+02;
3; Mismatches 0; Indels
  Score 60; DB 1; Length 199;
Pred. No. 1.03e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
                                                                                                                                                                                                                                                                       199 AA
                                                                                                                                                                                                                                                                         PRT;
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199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LACTERISTICS:
Lat 199 amino acids
LYPE: amino acids
STRANDEDNESS: Si-
TOPOLOGY:
LECULF
ALECULF
LACTERISTICS
LOCATION ACID
LECULF
LACTERISTICS
LACTER
                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.9%;
Similarity 70.0%;
7; Conservative
Query Match 29.9%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein LOCATION: 1..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Region
                                                                                                         129 LQARLDRLLR 138
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7 LQGRLQRLLQ 16
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|7 LQGRLQRLLQ 16
                                                                                                                                                                                                                                            us-08-792-019B-8
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:21:48 1999; MasPar time 4.63 Seconds 242.105 Million cell updates/sec Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-08-938-548B-12 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28

Scoring table:

PAM 150 Gap 15

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 30.698; Variance 52.943; scale 0.580 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

d. No.	77e+00	77e+00	77e+00	52e+00	02e+00	02e+00	02e+00	02e+00	00+e90	.06e+00	00+e90	.06e+00	06e+00	00+990	90e+00	90e+00	90e+00	38e+01	38e+01	38e+01	92e+01	92e+01	92e+01
Pred.	<u> </u>	H	, ,	۲,	ď.	5.	'n.	'n.		۲.	۲.	۲.	7	۲.	ο.	٠	٥.	4	H	ä	4	ij	H
Description	hypothetical protein	superoxide dismutase	superoxide dismutase	hypothetical protein	mALDP protein - mouse	membrane protein ydbH	hypothetical protein		hypothetical protein	transcription initiat	transcription initiat		transcription initiat	PAS1 protein - yeast	5		RNA-directed DNA poly	probable ABC transpor	adenylate cyclase (EC	fatty-acid synthase (hypothetical protein	proteinase 3 (EC 3.4.	hypothetical protein
ID	T00987	B41654	A41654	T02269	S47044	H64888	T00730	S23647	E69913	S11712	S41307	JN0443	JN0445	A55152	D69081	S49183	S19248	T02644	A33988	G01880	S25618	PRHU3	S51155
DB	7	~	7	N	7	7	7	7	~	7	~	7	7	7	~	~1	Н	7	7	7	7	Н	7
Length	145		187	511	736	879	1015	2115	178	442	510	525	528	1157	150	253	319	1420	69	2509	239	256	263
% Query Match	35.3	35.3	35.3	٠	ن	ω,	33.8	٠	ë.		33.3	ω,	33.3	3	32.8	•	2	•		32.3	31.8		31.8
Score	71	. 71	71	70	89	68	68	68	29	67	67	67	67	67	99	99	99	65	65	65	64	64	64
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S61858 A46101 BA6101 BA6101 S278C27 S278C27 A43917 S64616 S16239 A42115 A42115 A42115 A42115 A42115 A42115 A42115 A42115 A42115 A42115 A42115 A421105	ALIGNMENT	type comple protein T9 Arabidopsi #sequence r	tin, X	EMBL iana c tran tran c tran 25505;	2; 12 olecu	Score 7 Pred. N 8; Mi	DS 138 : AG 24	ype complete	Haemophilus pi sequence_revi	Langford, (1991) 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Conway, A.; Kurtz, D.; Oji, O.; Shen, Y.K.; Toriumi, M.; Vysotskaia, V.; Yu, G.; Davis, R.W.; Federspiel, N.A.; Theologis, A.; Ecker, J.R. submitted to the EMBL Data Library, April 1998 Genomic sequence for Arabidopsis thaliana BAC F22013.
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hypothetical protein F22013.25 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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#length 1015 #molecular-weight 111751 #checksum 6299
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#Litle The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
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##residues 1-879 ##label BLAT
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
A.; Braun, M.; Brignell, S.C.; Bron, S.; Borusillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.W.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.W.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Ehrlich, S.D.; Emmerson, P.T.; Foulger, D.; Fritz, C.; Fujita,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi,
G.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medique, C.; Medino, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medique, C.; Porvolik, S.; Prescort,
N.; Ogwa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porvolik, S.; Serson, E.;
Rey, M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.
Schowska, A.; Seror, S.J.; Serror, T.; Sachleich, S.; Schleich, S.; Schroethi, M.; Tamakoshi, A.; Tanaka, T.;
Takemaru, K.; Takenchi, M.; Tamakoshi, A.; Tanaka, T.;
Terpstra, P.; Tognoni, A.; Taosato, V.; Uchiyama, S.;
Wambutt, R.; Wedler, E.; Wedler, H.; Yamane, K.; Yasumoto,
Wilters, P.; Wipat, X.; Medler, E.; Wedler, H.; Yamane, K.; Yasumoto,
Wilters, P.; Wipat, X.; Yoshikawa, H.F.; Zumstein, E.;
Winters, P.; Wipat, Y.; Yoshikawa, H.F.; Zumstein, E.;
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##note the authors translated the codon GAG for residue 781 as
G1y, TTC for residue 1775 as Pro, and GGA for residue 2067 as G10.
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                                                                                                                                                                                                                                             #authors Yang, C.H.; Lambie, E.J.; Snyder, M.
#journal J. Cell Biol. (1992) 116:1303-1317
#title NuMA: an unusually long coiled-coil related protein in the mammalian nucleus.
#cross-references MUID:92176231
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#formal_name Bacillus subtilis
#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
24-Sep-1998
                          NuMA protein - human
#formal_name Homo sapiens #common_name man
19 Feb-1994 #sequence_revision 10-Nov-1995 #text_change
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#type complete
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##residues 1-2115 ##label YAN
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##molecule_type DNA
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#journal Gene (1992) 122:63-70
#title Four genes in Streptomyces aureofaciens containing a domain
characterstic of principal sigma factors.
#cross-references MUID:93083996
                                                                                                                                           #domain transcription initiation factor sigma katF
homology #label KTF
#length 525 #molecular-weight 57204 #checksum 9676
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#formal_name Streptomyces aureofaciens
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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#formal_name Pichia pastoris
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
10-Jul-1998
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J. Cell Biol. (1994) 127:1259-1273
Role of the PASI gene of Pichia pastoris in peroxisome
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   ##residues 1-525 ##label KOR
##cross-references GB:M90411; NID:9153305; PID:9153306
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##residues 1-528 ##label KOR
##cross-references GB:M90412; NID:g153308; PID:g153309
                                                                                                                                                                                                                   Score 67; DB 2; LA Pred. No. 7.06e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 2; L
Pred. No. 7.06e+00;
                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biogenesis.
#cross-references MUID:95050987
#accession A55152
                                                                                                                                                                                                               Query Match
Best Local Similarity 31.8%;
Matches 7; Conservative
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Best Local Similarity 36.4%;
Matches 8; Conservative
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                                                                         CLASSIFICATION
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#authors
#journal
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Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.; Gook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P. Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Vicaire, R. Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Caruso, A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.; McDougall, S.; Shimer, G.; Goyal, A.; Pietrokyski, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references GB:AE000920; GB:AE000666; NID:g2622729; PID:g2622730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein - Methanobacterium thermoautotrophicum (strain Delta H)
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deoxyuridine 5-triphosphate nucleotidohydrolase related
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Jun-1998
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                                                                                                                                                                                                                #region nucleotide-binding motif A (P-loop)\
#domain FtsH/SEC18/CDC48-type ATP-binding domain
homology #label VATP.
#region nucleotide-binding motif A (P-loop)
#length 1157 #molecular-weight 126983 #checksum 254C
                                                                                                      #Superfamily FtsH/SEC18/CDC48-type ATP-binding domain homology
ATP; P-loop; peroxisome biogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. (1997) 179:7135-7155
Complete genome sequence of Methanobacterium
thermoautotrophicum Delta H: functional analysis
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2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##experimental_source strain Delta H
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#cross-references MUD:98037514
#accession D69081
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                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 60.0%;
Matches 9: Control
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Best Local Similarity 50.0%;
Matches 9; Conservative
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10 RLQRLLQANGNHAAG 24
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(TM)	*****

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:22:38 1999; MasPar time 3.26 Seconds 242.897 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-12 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQRLLQANGNHAAGILIM 28 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:swissprot swiss-prot37 Database:

Variance 48.443; scale 0.652 Mean 31.574; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	6.21e-01	6.21e-01	1.33e+00	1.94e+00	1.94e+00	2.82e+00	2.82e+00	2.82e+00	4.07e+00	5.86e+00	5.86e+00	5.86e+00	5.86e+00	8.40e+00	8.40e+00	8.40e+00	8.40e+00	1.20e+01	1.20e+01	1.20e+01	1.20e+01	1.20e+01	1.20e+01
	Description	SUPEROXIDE DISMUTASE [SUPEROXIDE DISMUTASE [THYROID RECEPTOR INTER	ADRENOLEUKODYSTROPHY P	HYPOTHETICAL 96.8 KD P	NIFU PROTEIN.	RNA POLYMERASE PRINCIP	PEROXISOME BIOSYNTHESI	REGULATORY PROTEIN E2.	CUTICLE COLLAGEN 36.	COAT PROTEIN VP1.	SERINE/THREONINE PROTE	ADENYLATE CYCLASE (EC	INTERLEUKIN-11 PRECURS	MYELOBLASTIN PRECURSOR	SULFITE REDUCTASE (FER	OLIGOMYCIN RESISTANCE	HYPOTHETICAL 28 KD PRO	MITOCHONDRIAL 40S RIBO	MITOCHONDRIAL PEPTIDE	HYPOTHETICAL 63.2 KD P	PROBABLE SULFATE ADENY	HYPOTHETICAL 78.9 KD P
•	ID	SODC_HAEPA	SODC_HAEIN	TR12_HUMAN	ALD_MOUSE	YDBH_ECOLI	NIFU_FRAAL	HRDB_STRCO	PEX1_PICPA	VE2_HPV63	CC36_CAEEL	COA1_POVLY	AFSK_STRCO	CYAA_SCHPO	IL11_MOUSE	PRN3_HUMAN	SIR_SYNP7	YOR1_YEAST	YPE1_RHORU	RT04_YEAST	RF1M_HUMAN	YEAJ_ECOLI	NODQ_RHISB	YCBY_ECOLI
	DB	-	Н	Н	Н	Н	Н	٦	Н	Н	-	Н	Н	Н	Н		Н	П	Н	Н	~	П	H	7
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æ	Query Match	35.3	35.3	34.3	33.8	33.8	33.3	33.3	33.3	32.8	32.3	32.3	32.3	32.3			31.8	Ξ.	31.3	31.3	31.3	31.3	31.3	31.3
	Score	71	7.1	69	68	89	67	67	29	99	65	65	65	65	64	64	64	64	63	63	63	63	63	63
	Result No.		7	m	4	Ŋ	ø	7	ω	σ	10	11	12	13	14	15	16	17	18	19	. 20	21	22	23

NEGATIVE FACTOR (F-PRO 2.41e+01) HYPOTHETICAL OXIDOREDA 2.41e+01 HYPOTHETICAL OXIDOREDA 2.41e+01 FULMONARY SURFACTANT-A 2.41e+01 BETA-ARRESTIN 2. 2.41e+01 BETA-ARRESTIN 2. 2.41e+01 ADENOSYLHOMOCYSTEINASE 2.41e+01 LEGUMIN B PRECURSOR (B 2.41e+01 PHEROMONE B ALPHA 2 RE 2.41e+01 PROBABLE DNA PACKAGING 2.41e+01
RE 2.4
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FACCOLLEGGEN ALFRA Z(IV I./OCTOI HYDOTHERICAL DOORFIN M 2 A15401
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C 1
6(IV) C 1
RNA POLYMERASE SIGMA F 1.70e+01
TE SYNT 1
7
28.7 KD P 1
CAL PROTEIN K 1
ECDYSONE RECEPTOR (ECD 1.20e+01

STRAIN-1391;

MEDLINE; 92041655.

MEDLINE; 92041655.

"Copper-zinc superoxide dismutase of Haemophilus influenzae and H.
"Copper-zinc superoxide dismutase of Haemophilus influenzae and H.
parainfluenzae.";
J. BACTERIOL. 173:7449-7457(1991).
-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
-!- FUNCTION: MAY CONFER SURVINAL ADVANTAGE BY ACCELERATING
DISMUTATION OF SUPEROXIDE OF ENVIRONMENTAL ORIGIN TO HYDROGEN
PEROXIDE, DISRUPTIVE TO THE NORMAL MUCCCILIARY CLEARANCE PROCESS BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE; HAEMOPHILUS. 01-MAY-1992 (REL. 22, CREATED) 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) SUPEROXIDE DISMOTASE [CU-2N] PRECURSOR (EC 1.15.1.1). HAEMOPHILUS PARAINFLUENZAE SEQUENCE FROM N.A. PADDDARKEN PROCESS OF THE FEATURE OF

IN THE HOST

-:- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
-:- SUBUNIT: HOMODIMER.
-:- SUBCELLULAR LOCATION: PERIPLASMIC (POTENTIAL).
-:- SIMILARITY: BELONGS TO THE CU-2N SUPEROXIDE DISMUTASE FAMILY.

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EMBL; M84013; G148884; -,
PIR; B41654; B41654.

PROSITE; PS00087; SOD_CU_ZN_1; 1.
PROSITE; PS00323; SOD_CU_ZN_2; 1.
PFAM; PF00080; Sodcu; 1.
HSSP; P00446; 1YAI.
SYLDOREDUCTASE; COPPER; ZINC; PERIPLASMIC; SIGNAL.
SIGNAL 24 187 SUPEROXIDE DISMUTASE
CHAIN

POTENTIAL. SUPEROXIDE DISMUTASE [CU-ZN].

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MEDLINE; 95369734.
HARRIOTT O.T., HOSTED T.J., BENSON D.R.;
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                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                        MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION
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01-OCT-1996
   SCHERICHIA.
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                                      SEQUENCE FR
STRAIN=K12
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   Gaps
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-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). BELONGS TO THE MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: PROBABLE TRANSPORTER. COULD BE INVOLVED IN THE IMPORT OF VLCFA-COA SYNTHETASE INTO THE PEROXISOMAL MEMBRANE.-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-BINDING; GLYCOPROTEIN; TRANSMEMBRANE; TRANSPORT; PEROXISOME
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X-linked
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                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P52645; P77502; P76855; 01-00T-1996 (REL. 34, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 101-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) HYPOTHETICAL 96.8 KD PROTEIN IN LDHA-TYNA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches 10; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   SARDE C.O., THOMAS J., SADOULET H., GARNIER J.M., "CDNA sequence of Aldgh, the mouse homolog of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
ATP (BY SIMILARITY).
D373B00E CRC32;
   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; L
                                                                                                                                                                                   01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ADRENOLEUKODYSTROPHY PROTEIN HOMOLOG (ALDP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879 AA
   Mismatches
                                                                                                                                                      736 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:99672; ALDCH.
PROSITE; PSO0211; ABC_TRANSPORTER; 1.
PFAM; PF00005; ABC_LTAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            704 AGIPKMQGRLQELRQILGEAAAPVQPL 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PGPPGLQGRLQRLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81858 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            adrenoleukodystrophy gene."; MAMM. GENOME 5:810-813(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.8%;
Best Local Similarity 44.4%;
Matches 12; Conservative
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z33637; G520955; -.
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                                                                                                                                                      STANDARD;
                                     289 KPGPSGLQAKLASL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
258
353
493
                                                            TISSUE=FIBROTIC LIVER; MEDLINE; 95201443.
                                                                                                                                                                                                                                                                                  MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333
473
507
736 AA;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                     OR ALDGH.
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œ
                                                                                                                                                  ALD_MOUSE
P48410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDBH_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
SEQUENCE
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 Matches
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ID YL
AC PE
DT 001
DT 001
DE HI
GN YE
OS B
                                                                                                                                    RESULT
                                                                                                                                                  UNDER THE TEACH OF STANKING SERVICE STANKING SERVICE S
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                                                                                                                                                                                                                                                                                                                                                                          AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H., KASHIMOTO K., KIM S., KIMURA S., KITAGAWA M., KITAKAWA M., MAKINO K., MAKINO K., MAKINO K., MAKINO T., MOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMDEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.; SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                            BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES.J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUNCH P.K., MAT-JAN F., LEE N.A., DEAYALA B.A., CLARK D.P.; SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 1; Length 8/9;
Pred. No. 1.94e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; FRANKINEAE; FRANKIACEAE; FRANKIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> L (IN REF. 3).
8BFD7CF3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNPUBLISHED OBSERVATIONS (MAR-1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U36928; -; NOT_ANNOTATED_CDS.
ECOGENE; EG13180; YDBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 GVDGRLQAILQAHENELGDFVLHM 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 GLQGRLQRLLQANGNHAAG-ILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 36 I
879 AA; 96834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000235; G1787646; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-331 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 45.8%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D90776; G1742260;
D90777; G1742264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,
FROM N.A.
(12 / MG1655;
97426617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN CONFLICT 36
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LT 12
AFSK-GYRCO STANDARD; PRT; 799 AA. B54741; 01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
                                                         EMBL; L15418; G289662; -.
EMBL; U14685; G340271; ALT_INIT.
WORNER; C27H5 5; CE06893.
CUTICLE; CONNECTIVE TISSUE; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 KPGNQGLDPKAKPLLDKDGNYPVEV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RPGPPGLQGRLQRLLQANGNHAAGI 25
                                                                                                                                                                                                        30126 MW;
                                                                                                                                                                                                                                   32.3%;
                                                                                                                                                                                                                                                                                           214 PGPPGPAGQPGRVIQVNG 231
                                                                                                                                                                                                                                               Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                             2 PGPPGLQGRLQRLLQANG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COAT PROTEIN VP1.
LYMPHOTROPIC POLYOMAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; K02562; G333278; -. PIR; A03627; VVVP1L.
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                   150
187
226
257
295
                                                                                                                   89 1
118 1
167 1
194 2
231 2
260 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 86045879.
                                                                                                                                                                                                                                                                                                                                                                             COAl_POVLY
P04010;
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                               DOMAIN
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DOMAIN
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ID AE
AC P5
DT 01
DT 01
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                       ö
FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNNGGT-3') PRESENT
IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
WITH RECARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAULEY A.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: NEWATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.

-!- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE: 94131298.
LEVY A.D., KRAMER J.M.;
"Identification, sequence and expression patterns of the Caenorhabditis elegans col-36 and col-40 collagen-encoding genes.";
GENE 137:281-285(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                       EMBL; X70828; G312096; -.

PFAM; PF00508; E2_N; 1.

HSSP; PI7383; 1D4M.

EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; TRANS-ACTING FACTOR; DNA REPLICATION; REPRESSOR; NUCLEAR PROTEIN, SEQUENCE 398 AA; 45450 MW; C9BBOCEO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
                                                                                                                                                                                                                                                                                                                                                                                          Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Score 66; DB 1; Le
Pred. No. 4.07e+00;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
COL.-CCL.ECCL.ECGL.ES. 36.
COL.-36 OR C27H5.5.
CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 AA
                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR. SUBUNIT: BINDS DNA AS A DIMER.
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.8%;
Best Local Similarity 56.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 RSPPKGGQSRLRRLIQ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RPGPPGLQGRLQRLLQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                    REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC36_CAEEL
P34803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 86045879.
PAMLITA M., CLAD A., ZUR HAUSEN H.;
"Complete DNA sequence of lymphotropic papovavirus: prototype of a new species of the polyomavirus genus.";
VIROLOGY 143:196-211(1985).
-! SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 72 ICOSAHEDRAL UNITS,
EACH OF WHICH IS COMPOSED OF FIVE COPIES OF VPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; POLYOMAVIRUS
                                                                                                                                                                                                                                           FAMILY; COLLAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; July. Pred. No. 5.86e+00; ...matches 5; Indels
                                                                                                                                                                                                                                    REPEAT; MULTIGENE FAMILY
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
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HSSP; P49302; 1SIE.
LATE PROTEIN; COAT PROTEIN.
SEQUENCE 368 Aa; 40211 MW; 4979282C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9346DA48 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-0CT-1986 (REL. 02, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
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MEDLINE; 89315847
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                                                                                                                                                                                                                                                                                                                                                                                                          Three human
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J. EXP. MED.
[4]
                                                                                                                                                                                                                              GABAY J.E.; "Cloning of
                                                                                                                                                                                                                                                                                                                             SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                      JENNE D.E.;
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                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              9pter.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P24158; P15637;
01-APR-1990 (REL. 14, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3)
PRIN3 (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single mRNA.";
                                                                                                                                                                                                                                                                                                                                                                          MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;
"Molecular cloning and characterization of murine interleukin-11.";
EXP. HEMATOL. 24:1369-1376(1996).

1-F. FUNCTION: THIS PROTEIN STIMULATES PLASMACYTOMA PROLIFERATION,
T-CELL-DEPENDENT DEVELOPMENT OF IMMUNOGLOBULIN-PRODUCING B
CELLS AND SYNERGIZES WITH IL-3 IN SUPPORTING MURINE
MEGAKARYOCYTE COLONY FORMATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAB; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
LAMERDIN J.E., MCCREADY P.M., SKOWRONSKI E., ADAMSON A.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 199;
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MEDLINE; 92021028.
LABBAYE C., MUSETTE P., CAYRE Y.E.;
"Wegener autoantigen and myeloblastin are encoded by PROC. NATE. ACAD. SCI. U.S.A. 88:9253-9256(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 64; DB 1; Le
Pred. No. 8.40e+00;
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INTERLEUKIN-11.
1CB30772 CRC32;
                                                                                                                                                               (REL. 33, CREATED)
(REL. 33, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
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CYTOKINE; GROWTH FACTOR; SIGNAL.
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larity 53.3%;
Conservative
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               PVQLQGRLERLIKS 1552
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                                                                                                                                STANDARD;
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                                                   PPGLQGRLQRLLQA 17
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IL11_MOUSE
P47873;
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01-FEB-1996 (
01-NOV-1997 (
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loning of cDNA for proteinase 3: a serine protease, antibiotic, and toantigen from human neutrophils."; EXP. MED. 172:1709-1715(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WILDE C.G., SNABLE J.L., GRIFFITH J.E., SCOTT R.W.; "Characterization of two azurphil granule proteases with active-site homology to neutrophil elastase.":
               STILWAGEN S.,
BURKHART-SCHULTZ K.J., GORDON L., KYLE A., RAMIREZ M., STILWAGEN S., PHAN H., VELASCO N., DO L., REGALA W., TERRY A., GARNES J., DANGANAN L., POUNDSTONE P., CRISITENSEN M., GEORGESCU A., AVILA J., LIU S., ATTIX C., ANDRRIES T., TRANKHEIM M., AMICO-KELLER G., COEFIELD J., DUARTE S., LUCAS S., BRUCE R., THOMAS P., QUAN G., KRONMILLER B., ARELLANO A., MONTGOMERY M., OW D., NOLAN M., TRONG S., SUBMITLED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 91079774.
CAMPANELLI D., MELCHIOR M., FU Y., NAKATA M., SHUMAN H., NATHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in the
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 2-256 FROM N.A., AND SEQUENCE OF 48-71 AND 156-181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of proteinase-3 (PR-3), a neutrophil serine proteinase. Structural and functional properties."; J. BIOL. CHEM. 266:9540-9548(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAO N.V., WEHNER N.G., MARSHALL B.C., GRAY W.R., GRAY B.H.
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GUPTA S.K., NILES J.L., MCCLUSKEY R.T., ARNAOUT M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROC. NATL. ACAD. SCI. U.S.A. 89:8215-8219(1992).
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J. BIOL. CHEM. 265:2038-2041(1990).
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MEDLINE; 90130450.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:23:12 1999; MasPar time 6.52 Seconds 234.276 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-12 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQARLQANGNHAAGILIM 28

Description: Perfect Score: Sequence: Title:

PAM 150 Gap 15 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 30.180; Variance 51.706; scale 0.584 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length	DB	ID	Description	Pred. No.
7	201	100.0	130	11	055241	HYPOCRETIN (PREPRO-ORE	4.74e-26
7	201	100.0	130	11	055232	PREPRO-OREXIN.	4.74e-26
m	197	98.0	131	Ø	077668	PREPRO-OREXIN PRECURSO	3.52e-25
4	190	94.5	131	4	043612	PREPRO-OREXIN.	1.15e-23
Ŋ	16	37.8	1174	9	095168	TIGHT JUNCTION PROTEIN	2.98e-01
9	. 75	37.3	1277	11	035821	PAR INTERACTING PROTEI	4.31e-01
7	73	36.3	249	11	P97382	K+ CHANNEL BETA4 SUBUN	8.98e-01
80	71	35.3	145	10	048721	T9J22.21 PROTEIN.	1.85e+00
σ	7.0	34.8	511	10	080740	T13D8.6 PROTEIN.	2.64e+00
10	69	34.3	331	13	091640	LEUCINE ZIPPER WITH BA	3.76e+00
11	69	34.3	389	Π	088539	WW DOMAIN BINDING PROT	3.76e+00
12	68	33.8	162	7	085680	RNA POLYMERASE SIGMA-L	5.34e+00
13	68	33.8		m	042651	HYPOTHETICAL 55.5 KD P	5.34e+00
14	89	33.8		10	064673	F22013.25.	5.34e+00
15	68	33.8	2115	4	014980	NUMA PROTEIN.	5.34e+00
16	67	33.3	161	7	085683	RNA POLYMERASE SIGMA-L	7.55e+00
17	67	33.3	178	7	031955	YONC PROTEIN.	7.55e+00
18	67	33.3	178	σ	064066	HYPOTHETICAL 19.6 KD P	7.55e+00
19	67	33.3	413	11	035141	MAXP1.	7.55e+00
20	67	33.3	462	7	P95644	RNA POLYMERASE SIGMA F	7.55e+00

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ALIGNMENTS

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TISSUE-BRAIN;
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080740;
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048721;
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PAR INTERACTING PROTEIN.
RATTUS NORVEGICUS (RAT).
EUKARYOTA, METAZOA; CHORDATA, VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MAINAE; RATTUS.
                                                       SEQUENCE FROM N.A.
MEDLINE; 96421547.
BEATCH M., JESAITIS L.A., GALLIN W., GOODENOUGH D.A., STEVENSON B.R.;
"The tight junction protein ZO-2 contains three PDZ
(PSD-95/Discs-Large/ZO-1) domains and an alternatively spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE: 91084854.
WUARIN J., SCHIBLER U.;
"Expression of the liver-enriched transcriptional activator protein
DBP follows a stringent circadian rhythm.";
CELL 63:1257-1266(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 37.8%; Score 76; DB 6; Length 1174 Best Local Similarity 32.1%; Pred. No. 2.98e-01; Matches 9; Conservative 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
COMTE P.A., OSSIPOW V., SCHIBLER U.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                         GOODENOUGH D.A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                          EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                         DECLEM M.; SERICH M.; SUBMITTED (AUG-1996) TO EMBL/GENBANN, LL 127152; G1536970; -. PFAM; PF00559; PDZ; 3. PFAM; PF00625; Guanylate_kin; 1. PFAM; PFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U83590; G2253211; -
SEQUENCE 1277 AA; 144674 MW; 89721F79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 RSPSPELRGRPDHAGQPDSDRPIGVLLM 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOL. CHEM. 271:25723-25726(1996)
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  tumor suppressor protein.";
J. CELL BIOL. 124:949-961(1994).
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P97382;
P97382;
01-MAY-1997 (TREMBLREL. 03, CI
01-MAY-1997 (TREMBLREL. 03, LA
01-NOV-1998 (TREMBLREL. 08, LA
K+ CHANNEL BETA4 SUBUNIT.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.3%;
Similarity 29.6%;
8; Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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035821
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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VYSOTSKAIA V.S., SCHWARTZ J.R., KWAN A., TORIUMI M., YU G., OJI, O,
LIU S., LI J., ARAUJO R., AU M., BRENDEL V., BUEHLER E., CONWAY A.B.,
CONWAY A.R., DEWAR K., FENG J., KIM C., KURIZ D., LI Y., PALM C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                      MEDLINE; 96421640.
FINK M., DUPRAT F., LESAGE F., HEURTEAUX C., ROMEY G., BARHANIN J., LAZDUNSKI M.;
"A new K+ channel beta subunit to specifically enhance Kv2.2 (CDRK)
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                            Length 249;
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Pred. No. 8.98e-01;
....arrohes 2; Indels
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LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                               249 AA; 27749 MW; 8805DBE7 CRC32;
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EMBL; U65593; G1695272; -.
IONIC CHANNEL.
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                      SCIUROGNATHI; MURIDAE; MURINAE; MUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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2 PGPPGLQGRLQRLLQANGNHAAG 24
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08°,
08°,
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01-NOV-1998 (TREMBLREL.
T13D8.6 PROTEIN.
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                                                              SEQUENCE FROM N.A.
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Search completed: Fri Aug 20 21:23:53 1999 Job time : 41 secs.
1 RPGPPGLQGRLQRLLQAN 18
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NUMA PROTEIN.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                             01-40G-1998 (TREMBLREL. 07, CREATED)
01-40G-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-40G-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
10-40G-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
F22013.25.
ARABIODPSIS THALIANA (MOUSE-EAR CRESS)
EUKARYOTA, VIRIDIPLANTAE, STREATOHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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SEQUENCE FROM N.A.
MEDLINE; 92176231.
YANG C.H., LAMBIE E.J., SNYDER M.;
"NUMA: an unusually long coiled-coil related protein in the mammalian
"NUMA: _ ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94013066.

MEDLINE; 94013066.

MEDRINE; 94013066.

MAERAWA T., KURIYAMA R.;

Primary structure and microtubule-interacting domain of the SP-H
antigen: a mitotic MAP located at the spindle pole and characterized
as a honologous protein to NuMa.";

CELL SCI. 105:589-600(1993).

EMBL; 211583; G35119; -

CONFLICT 124 124 Q -> P (IN REF. 2).

CONFLICT 1587 1587 0 -> P (IN REF. 2).

SEQUENCE 2115 AA; 238273 MW; 81A36BA3 CRC32;
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SHINN P., BUEHLER E., DEWAR K., FENG J., KIM C., LI Y., SUN H.,
CONWAY A., COWMAY A., KURTZ D., OJI O., SHEN Y.K., TORIUMI M.,
VICTISKAIA V., YU G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
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Pred. No. 5.34e+00;
6; Mismatches 3; Indels
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECKER J.R.; SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AC03981; G3063465; -. SEQUENCE 1015 AA; 111751 MW; 82FA3G3F CRC32;
                                                                                                                                                                                                                                              PRT; 1015 AA
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Best Local Similarity 50.0%;
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                                                        280 LQEVLQSDSNHVPSVLT 296
Conservative
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Q14980;
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064673
064673;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Aug 20 21:14:33 1999; MasPar time 8.03 Seconds 325.686 Million cell updates/sec

Tabular output not generated.

Title: >US-08-938-548B-10
Description: (1-123) from US08938548B.pep
Perfect Score: 899
Sequence: 1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTTALAPRGGSGV 123

Sequence: 1 VPWAAVTLLLI Scoring table: PAM 150

Scoring table: PAM 150

Gap 11

Searched: 170751 segs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part39 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Statistics: Mean 29.551; Variance 129.928; scale 0.227

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	o 1.08e-73	3.25e-73	2.79e-69	2.79e-69	o 6.74e-58	v 4.05e-01	v 4.05e-01	1 4.05e-01	e 4.05e-01	e 4.05e-01	L 4.05e-01	7.98e+00	7.98e+00	7.98e+00	7.98e+00	7.98e+00
Description	Mouse HFGAN72 recepto	Mouse hypocretin 35.	Rat hypocretin 35.	Rat HFGAN72 receptor	Human HFGAN72 recepto	Glial cell line-deriv	Glial cell line-deriv	A GDNFR-alpha-related	Human GDNF alpha-3 re	Human GDNF alpha-3 re	Human Ret ligand RetL	Human fibulin type 1	Fibulin A.	Fibulin B.	Human fibulin type 1	Fibulin C.
ID	W61383	W50158	W50157	W61382	W61381	W84185	W84186	W84180	W65116	W65117	W37463	W27598	R11148	R11149	W27599	R11150
DB	33	30	30	33	33	39	39	39	32	32	28	28	ď	7	28	~
Query Match Length DB	123	130	130	130	131	378	400	400	400	400	400	556	266	601	601	683
Query	100.0	99.4	94.9	94.9	81.6	12.6	12.6	12.6	12.6	12.6	12.6	10.7	10.7	10.7	10.7	10.7
Score	899	894	853	. 853	734	113	113	113	113	113	113	96	96	96	96	96
Result No.		7	ю	4	Ŋ	9	7	8	6	10	11	12	13	14	15	16

0.0000000000000000000000000000000000000	7.01e+01 7.01e+01 7.01e+01
fibulin ty fibulin ty al recombin lecithin-co N-proteina e human cho N-proteina e human cho A-1BB liga A-1BB liga aspartic p napsin A p napsin	Human Ilt3-ligand. Human S86/S109 Flt3 l S. clavuligerus ORF1
72774447779785577718557777777777777777777777777	W67769 R66175 R77858
228 228 333 333 333 333 333 333 333 333	13
2083 4400 4440 12111 12114 12114 1111 111	ກຕນ
00010111 00000000000000000000000000000	
00000000000000000000000000000000000000	2 CO CO
	4 4 4 2 4 7

ALIGNMENTS

RESULT

ID W61883 standard; Protein; 123 AA.

W 61883; standard; Protein; 123 AA.

W 61883; standard; Protein; 123 AA.

W 61883; standard; Protein.

W MFGAN72 receptor protein.

W MFGAN72 receptor protein.

W MFGAN72 receptor protein:

W MFGAN72 receptor; angina pectoris; myocardial infarction; psychotic disorder; os mus sp.

Location/Qualifiers

FT Region Si3..65

Mus sp.

Location/Qualifiers

FT Region G9.96

Mote= "Ligand 72A"

FT Region G9.93093

PF 17-DEC-1997; 19-93993

PF 17-DEC-1997; 19-93993

PR 17-DEC-1997; 19-93993

PR 17-DEC-1997; 19-887382.

PR 18-MR 19-88174672229.

PR 18-MR 19-88174677229.

PR 18-MR 19-88174672229.

PR 18-MR 19-88174677229.

PR 18-MR 19-88174677229.

PR 18-MR 19-881747677229.

PR 18-MR 19-MR 18-MR 1

US-08-938-548B-10.rag

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The HFGAN72 receptor protein contains two ligands whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bulimia, cachexia, chronic renal failure, remain disease, congestive heart failure, impaired glucose tolerance and sexual disease, congestive heart failure, impaired glucose tolerance and sexual disease, congestive heart failure, impaired glucose tolerance and sexual disease, in the HFGAN72 receptor ligand is useful for treating e.g. batterial, fungal, protozoan and viral infections, particularly infections caused by HTV-1 or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthm, parkinson's disease, both acute and congestive heart failure, hypotension, hypotension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign prostatic hypertrophy, chronic renal failure, renal disease, impaired glucose tolerance, sexual dysfunction and psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glial cell line-derived neurotrophic factor receptor gamma 1.
Glial cell line-derived neurotrophic factor receptor gamma 1;
GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gammal
Parkinson's disease; schizophrenia; insomnia; tardive dyskenisia;
hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
renal disorder; kidney failure; gut dysfunction; regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated glial cell derived neurotrophic factor receptors - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 734; DB 33; Length 131;
Pred. No. 6.74e-58;
12; Mismatches 10; Indels 1
                                                                   HFGAN72 receptor ligands - and corresponding DNA, agonists
  Brooks DP, Gellai M, Wilson S, Yanagisawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361..378
/note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease or Gilles dela Tourett's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
Gentz RL, HSU T, Ni J, Ruben SM, Young P;
WPI; 99-070150/06.
N-PSDB; V99333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32..378 //label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W84185 standard; Protein; 378 AA
                                                                                              etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 81.6%;
Best Local Similarity 81.5%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W84185;
25-MAR-1999 (first entry)
                                                                                         antibodies, antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32..360
/note= "
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20-MAY-1998, U10328.
27-JUN-1997; US-884638.
20-MAY-1997; US-047092.
                        98-324672/29.
                                           N-PSDB; V28138
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Claim 5: Fig 4: 35pp: English.

Claim 5: Fig 4: 35pp: English.

The HFGANZ receptor protein contains two ligans whose antagonists can be used for treating obesity, diabetes, anorexia nervosa, bulimia, cachexia, chronic renal failure, renal disease, congestive heart failure, impaired glucose tolerance and sexual dysfunction. The agonist is useful for treating anorexia nervosa, bulimia and cachexia. The HFGANZ receptor ligand is useful for treating e.g. bacterial, fungal, protezoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, anorexia nervosa, bulimia, cachexia, obesity, diabetes, asthma, parkinson's disease, both acute and congestive heart failure, asthma, pertoris, myocardial infarction, ulcers, asthma, allergies, benign pectoris, myocardial infarction, ulcers, asthma, allergies, benign construction processing pertorion; and dysfunction and psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delirium, demential, severe mental retardation and dyskinesias such as Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-0CT-1998 (first entry)

Human HFGAN72 receptor protein.

HFGAN72 receptor; eating disorders; renal disease; heart failure; sexual dysfunction; HIV; cancer; Parkinson's disease; urinary retention; osteoporosis; angina pectoris; myocardial infarction; psychotic disorder; neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 rrpgppglqgrlqrllqangnhaagiltmgrragaelepypcpgrrcptatalaprgg 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VPWAAVTLILLILPPALLSLGVDAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLGK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vpwaavtlllllllppallslgvdagplpdccrqktcscrlyellhgagnhaagiltlgk 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 130;
                                                                                                                                                                                                                                                      receptor ligands - and corresponding DNA, agonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. (SMIK ) SMITHKLINE BEECHAM PLC. Bergsma DJ, Brooks DP, Gellai M, Wilson S, Yanagisawa M; WPI; 98-324672/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 853; DB 33;
Pred. No. 2.79e-69;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease or Gilles dela Tourett's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
34..66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Ligand 72A"
70..97
/note= "Ligand 72B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 131 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cch 94.9%;
al Similarity 95.1%;
117; Conservative
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17-DEC-1997; 310216.
26-SEP-1997; US-939093.
17-DEC-1996; US-033604.
19-MAR-1997; US-820319.
02-JUL-1997; US-887382.
                                      26-SEP-1997; US-939093.
17-DEC-1996; US-033604.
19-MAR-1997; US-820519.
02-JUL-1997; US-887382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                                N-PSDB; V28139
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                                                                                                                                                                                                                                                   HFGAN72
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Matches

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GDNFR-gammal;

W61381

121

Region Region

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10; Indels 1; Gaps

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cells, especially tumours.
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                  28-SEP-1998 (first entry)

Human GDNF alpha-3 receptor protein #1.

Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;

treatment; neurodegenerative disasse; Parkinson's Disease; ALS; SMA;

amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;

Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1998 (first entry)

Human GDNF alpha-3 receptor protein #2.

Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;

treatment; neurodegenerative disease; Parkinson's Disease; ALS; SNA,

amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;

Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;

muscular dystrophy; diagnostic.
                                                                                                                                                                                                                                                                                                             This sequence represents a novel glial cell line-derived neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be used to frreat e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases (including the muscular dystrophies) and nerve and sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New factor alpha 3 receptor polypeptide and e.g. DNA and agonists used to treat neuro degenerative diseases, muscular diseases and nerve and muscle trauma and in diagnostic assays claim 13; Fig 4; 22pp; English.
                                                                                                                                                                                                                                                                  New factor alpha 3 receptor polypeptide and e.g. DNA and agonists sused to treat neuro degenerative diseases, muscular diseases and nerve and muscle trauma and in diagnostic assays claim 4; Fig 2; 22pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 113; DB 32; Length 4 up Pred. No. 4.05e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 plppvvlmlllllppsplplaa-gdplptesrlmn-sc
                                                                                                                                                    /note= "Partial sequence"
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                                                                                                                          1. 400
/label= GDNF alpha-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= GDNF alpha-3
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W65117 standard; Protein; 400 AA.
W65116 standard; Protein; 400 AA
                                                                                          muscular dystrophy; diagnostic.
                                                                                                                                                                                  20-NOV-1997; 309375.
09-MA-1997; 62-009463.
27-NOV-1996; GB-024677.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-NOV-1996; GB-024677.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.6%;
Best Local Similarity 47.4%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1997; 309375.
09-MAY-1997; GB-009463.
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                                                                                                      Homo sapiens
                                                                                                                                                            EP-846764-A2
                                                                                                                                                                                                                                 Lawrence GMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                            Protein
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Claim 2: Page 85-86; 113pp; English.

This amino acid sequence comprises human Ret ligand (RetL) RetL3, and conducted from a adult heart and cond controls. Ret and human RetL1, human RetL2 and mouse RetL3 sequences (see W07457-62) are also claimed. Human RetL3 is 3.3% identical to human RetL1, 34.9% identical to human RetL3. RetL3 and 76.8% identical to murine RetL3. Ret ligand is a key component of the Ret signalling pathway that specifically interacts with Ret receptor protein, triggering Ret dimerisation and/or autophosphorylation of the Ret tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic or eukaryotic host cally transformed or transfected with these vectors are claimed, as well as a method for production of RetL3, its soluble variants and fusion proteins with a toxin, imageable compound or radionuclide. RetL3, optionally when expressed from vectors in vivo, is used to promote growth of new tissue and survival of damaged tissue, particularly kidney or neural tissue. Typical applications are in renal failure, nephritis, kidney transplants, toxic or hypoxic injury, neurodegeneration, moctor neurone disease, multiple sclerosis, bacterial, viral or prion infections (e.g. meningitis, myelopathy associated with HIV or creutzfeldt-Jakob disease), cranial nerve or spinal cord injury, developmental disorders such as Down's syndrome system (Lyme disease, muscular dystrophy and myasthenia gravis).

Fusion proteins are used to deliver toxins etc. to Ret-expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
This sequence represents a novel glial cell line-derived neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat e.g. neurodegenerative diseases (such as ParkInson's Disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neurophy (SMA), muscular diseases (including the muscular dystrophies) and nerve and such erroma and in diagnostic assays for such conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding ret receptor ligands and related proteins vectors, transformed cells and antibodies, used for promoting cell growth and improving survival of injured cells, especially renal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1998 (first entry)

Ruman Ret ligand RetL3.

Ret ligand, RetL3 receptor; signal transduction; human; cell growth; renal cell; nerve cell; renal failure; nephritis; kidney transplant; toxic injury; hypoxic injury; neurodegeneration; motor neurone disease; multiple sclerosis; infection; moningitis; myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                     Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                         Score 113; DB 32; Le
Pred. No. 4.05e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PWAAVTLILLILLILPPALLSLGVDAQPLPDCCRQKTCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 plppvvlmlllllppsplplaa-gdplptesrlmn-sc
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27-NOV-1997.

10-APR-1997, U5-017427.

08-MAY-1996; U5-017427.

07-JUN-1996; U5-019300.

16-JUL-1996; US-021859.

(BIOJ ) BIOGEN INC.

Cate RL, Hession C, Sanicola-Nadel M;

WPF; 98-018411/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W37463 standard; Protein; 400 AA W37463;
                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.6%;
Best Local Similarity 47.4%;
Matches 18; Conservative
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WO9744356-A2.
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Purified fibulin, DNA encoding it and antibodies reactive with it useful as diagnostic and therapeutic component.

Sclaim 10; Fig 4; 56pp; English.

Claim 10; Fig 4; 56pp; English.

The fibulin A, B and C forms are identical from their N-terminals to a divergence point at poss. 566 (terminal codon in fibulin A)

and divergence point at poss. 566 (terminal codon in fibulin A)

and 683 residues resp. All three forms are rich in cysteine (11 %) and analysis with on. and spacing of the Cys residues revealed two cys research of the Cys residues revealed two cys residues. The same motif is found in a possible and the cysteine (11 %) and possible acking two Cys residues. The same motif is found in albumin, vitamin D-binding protein and alpha fetoprotein. The type II motif, related to repeats found in epidermal growth catcor precursor is a 6-Cys pattern repeated in the times, although the ninth repeat in the A form is incomplete. Four of the repeats, (2, 3, 4 and 9) differ from the EGF-like motif in having a 4-6 consensus sequence consensus O-glycosylation sequence, CXCXCC.

Immediately following each repeats is a pentapeptide with the consensus sequence XD(I/V)(D/N)E. Fibulin binds to the cytor reconstrict in a pation dependent branch consensus of plasmic domain to fit he warm of the repeat of the cytor or a plasmic domain of the betal submit of integrin adhesion the presented or plasmic domain of the betal submit of integrin and so the cytor or contains and so the cytor or contains and so the presented the presented to the plant of the betal submit of integrin and so the cytor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses. See also R11147, R11148 and R11150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human fibulin type 1 isoform (variant B).
Human fibulin protein; met-OB protein; hypertension; obesity;
isoform; type II diabetes; fibrogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 10.7%; Score 96; DB 2; Length 601; Local Similarity 57.1%; Pred. No. 7.98e+00; les 16; Conservative 3; Mismatches 8; Indels
           /label= consensus pentapeptide
                                                                                                                                                                                          /label= consensus pentapeptide
                                                                                                    consensus pentapeptide
                                                     /label= repeat unit 7
480..484
                                                                                                                                           /label= repeat unit 8
530..535
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W27599 standard; Protein; 601 AA.
W27599;
                                                                                                                                                                                                                                                                                18-AUG-1989; US-395773.
(LJOL-) LA JOLLA CANCER RES.
(AMNA-) AMER NAT RED CROSS.
                                                                                                                                                                                                                                                                                                                                               Ruoslahti EI, Argraves WS;
WPI; 91-087250/12.
N-PSDB; Q11009.
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                                                                                                                      .529
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03-APR-1997; U06280.
04-APR-1996; US-627636.
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Bennett LG;
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WO9738014-Al.
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single residue. Embodied within repeats 5, 6, 7 and 8 is the consensus sequence for Asp and Asn hydroxylation. The 7th repeat contains the consensus O-glycosylation sequence, CXCXFC.
Immediately following each repeat is a pentapeptide with the consensus sequence XD(I/V)(D/N)E. Fibulin binds to the cytoplasmic domain of the betal subunit of integrin adhesion receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, laminin, and possibly also other proteins. Antibodies reactive suit the protein have important diagnostic and therapeutic uses. See also RIL147, RIL149 and RIL150.
                                                                                                                                                                                                                                                                                Score 96; DB 2; Length >vo, Pred. No. 7.98e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        integrin; adhesion; receptor; fibronectin.
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/label= repeat unit 2
261..265
/label= consensus pentapeptide
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180..566
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/label= repeat unit 6
440..44
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307..311
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                                                                                                                                                                                                                                                                                                                                                                                                                     'label= type I motif
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/label= fibulin B
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R11149 standard; Protein; 601 AA.
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ilarity 57.1%;
Conservative
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21-MAY-1991 (first entry)
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:16:02 1999; MasPar time 8.37 Seconds 588.583 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-10 (1-123) from USO8938548B.pep 899 1 VPWAAVTLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123 Title:

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

122810 seqs, 40068593 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 40.175; Variance 83.764; scale 0.480

Statistics:

SUMMARIES

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Result No.	Score	Query	Query Match Length	DB	ΩI	Description	Pred. No.
-	106	11.8	629	7	C71413	hypothetical protein	1.65e-02
2	101	11.2	131	Н	SEPG	secretin precursor -	7.73e-02
m	96	10.9	641	8	A45054	probable intercellula	1.91e-01
4	96	10.7	601	~	B36346	fibulin 1 precursor,	3.46e-01
Ŋ	96	10.7	683	~	C36346	fibulin 1 precursor,	3.46e-01
9	92	10.2	838	7	145557	eyeless, long form -	1.11e+00
7	91	10.1	440	Н	XXHUN	phosphatidylcholine	1.48e+00
80		10.1	602	~	S39782	cyclooxygenase 1 - ra	1.48e+00
6	89	6.6	602	~	S69198	prostaqlandin G/H syn	2.61e+00
10	88	9.9	1061	1	OYHUAR	natriuretic peptide r	2.61e+00
11	8	6.6	1321	7	T00382	hypothetical protein	2.61e+00
12	88	9.8	226	7	A70565	probable cutinase pre	3.46e+00
13	88	9.8	245	7	S43293	FLT3/FLK2 ligand (clo	3.46e+00
14	88	•	254	~	I38427	4-1BB ligand - human	3:46e+00
15	88		438		XXMSN	phosphatidylcholine	3.46e+00
16	88	8.6	491		JC6197	stromelysin 3 (EC 3.4	3.46e+00
17	87	9.7	252		B70602	hypothetical protein	4.57e+00
18	87	9.7	583		I50518	DNA binding protein E	4.57e+00
19		9.7	599		A36746	prostaglandin-endoper	4.57e+00
20		9.6	322	7	G64151	hypothetical protein	6.03e+00
21	86	9.6	410		S74705	hypothetical protein	6.03e+00
22	86	9.6	440	7	JC1502	phosphatidylcholine	6.03e+00
23	86	9.6	497	7	S43745	phosphatidylinositol-	6.03e+00

complement C3 precurs 6.03e+00 placental lactogen pr 7.93e+00 triacylglycerol lipas 7.93e+00 triacylglycerol lipas 7.93e+00 ferric enterobactin t 7.93e+00 hypothetical protein 7.93e+00 collagen alpha chain 7.93e+00 gene E protein - phag 1.04e+01 lysis protein - phag 1.04e+01 lysis protein - phage 1.04e+01 lysis protein 108 precursor 1.04e+01 lERK-3 - human 1.04e+01 lERK-3 - human 1.04e+01 lutropin-choriogonado 1.04e+01 lutropin-choriogonado 1.04e+01 lutropin-choriogonado 1.04e+01 lutropin-choriogonado 1.04e+01 dTpase-activating pro 1.04e+01 lutropin-choriogonado 1.04e+01 lutropin-mouse	S e rabidopsis	sis thalia revision	I.; Bent, E.; Love, K.; Goodman, H.; R.; Dirkse, W.; Van Staveren, M.; L.; Ridley, P.; Hudson, S.A.; Patel, angger, T.; Pohl, T.; Medler, E.; negger, T.; Pohl, T.M.; Terryn, N.; Oel, R.; De Clerck, R.; Van Montagu, M.;	Lecharny, A.; Auborg, S.; Gy, I.; Krels, M.; Lao, N.; Kavanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.; Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, P.; Douka, A.; Voukelatou, E.; Milioni, D.; Hatzopoulos, P.; Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Pelme, K.; Benes, V.; Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny, M.; Voet, M.; Volckaert, G.; Mewes, H.W.; Klosterman, S.; Schueller, C.; Chaluatzis, N.	-488 contiguous sequence from chromosome 4 lana.	leic acid sequence not shown; ot shown	y :D:g2244829; PID:è326841; PID:g2244855 .ar-weight 74635 #checksum 9028	e 106; DB 2; Length 679; . No. 1.65e-02; Mismatches 22; Indels 4; Gaps 4;	KYCRSK-YETIHGONHDNAADVLELAIKREMPAELL-R-ASLRHTNEDORNFLLNVGRSA 654
1 C3RT 2 A37930 2 S57275 2 S16296 2 T00728 2 C00728 2 C00	AL type prot	#	98 Bancroft, Bergkamp, W.; Drost Y, G.; Pif R.; Weitze	A.; Aubor T.; Hempe Ter, M.; Montfort atou, E.; E.; Ober ; Jones, ; Ansorg M.; Volck	8) 391:485-48 1.9 Mb of co opsis thaliar 121113	inary; nuclesslation not	##label BEV Z97337; NID 5 #molecula	8%; Score 3%; Pred. ve 16;	ADVLELAIK : : : AGILTLGKR
1663 236 236 317 317 317 915 102 102 102 102 103 115 223 323 325 326 327 327 328 331 331 331 338 338 338 338 338 338 33	C71413 #	#Iormal_name cress columbia 03-Aug-1998	05-bec-195 C71413 Bevan, M.; E Bevan, C.; Stiekema, K.; Murphy Wambutt, F	Lecharny, A., Kavanagh, T., Ka, Schaedar, James, R.; Mc A.; Voukelart Piravandi, E. Moores, T.; C. Rechman, S.; M.; Voet, M.;	Analysis of of Arabido	413 prelim tran	LYPE DNA 1-679 # erences GB:2 4COP9-4G3845 #length 679	11.8 arity 32.3 Conservativ	THGQNHDNA - :: THGAG-NH
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                                                                                                                                                                                                                                                                                                                                                          #authors Argraves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E.
#journal cell (1989) 58:623-629
#title Fibulin, a novel protein that interacts with the fibronectin receptor beta-subunit cytoplasmic domain.
#cross-references MUID:89354537
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Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
Science (1994) 265:785-789
Homology of the eyeless gene of Drosophila to the Small eye
gene in mice and Aniridia in humans [see comments].
                                                                                    #authors Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
#journal J. Cell Biol. (1990) 111:3155-3164
#title Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure.
#cross-references MUID:91100426
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#product fibulin 1 splice form C #status predicted
#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 683 #molecular-weight 74475 #checksum 7443
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#formal_name Drosophila melanogaster
09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change
19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 10-Sep-1997
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Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession C36346
##molecule_type mRNA
##residues 1-683 ##label ARG
##cross_references GB:X53743; NID:g31418; PID:g31419
                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
##residues 1-566 ##label AR2
##cross-references GB:X53741; NID:g31414; PID:g31415
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#map_position 22q13.3-22q13.3
KEYWORDS alternative splicing; glycoprotein
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Pred. No. 3
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                                               C36346; A36346; A32826
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Best Local Similarity 57.1%;
Matches 16; Conservative
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#authors
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Rogne, S.; Skretting, G.; Larsen, F.; Myklebost, O.; Mevag, B.; Carlson, L.A.; Holmquist, L.; Gjone, E.; Prydz, H. Biochem. Biophys. Res. Commun. (1987) 148:161-169
The isolation and characterisation of a CDNA clone for human lecithin:cholesterol acyl transferase and its use to analyse the genes in patients with LCAT deficiency and fish
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#title The isolation and characterisation of cDNA and genomic clones
for human lecithin:cholesterol acyltransferase.
#cross-references MUID:88050946
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Waterfield, M.D.; McIntyre, N.; Williamson, R.; Humphries,
                                                                                                                                                                                                                                                                                                                                                                                                             XXHUN #type complete
phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
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04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
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A00571; A25575; A29661; JQ0036; A29133; I52260; A28511
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#title Human lecithin-cholesterol acyltransferase gene: compleross-references MID:87091568
#accession A25575
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##residues 17-256,'H',258-440 ##label TAT
##cross-references GB:X06537; NID:g34284; GB:M26268; NID:g187024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor - human
lecithin--cholesterol acyltransferase precursor;
phospholipid--cholesterol acyltransferase precursor
                                                           392
                                                                                                                                                                                                                                    731
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#domain paired box homology #label PBH\
#domain homeobox homology #label HOX
th 838 #molecular-weight 87662 #checksum
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                                                                                                                   Length 838;
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NCE A25575
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##cross-references GB:X04981; NID:g34286; PID:g34287
                                                                                                                Score 92; DB 2; Le
Pred. No. 1.11e+00;
19; Mismatches 17
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#accession A29661
                                                                                                                Query Match 10.2%;
Best Local Similarity 28.3%;
Matches 15; Conservative
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#length 838
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##residues 13-44
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the authors translated the codon CAT for residue 241 as

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Gaps

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Length 1321;

Score 89; DB 2; Length 1321 Pred. No. 2.61e+00; 5; Mismatches 7; Indels

Pred.

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Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. (1998) 5:169-176
Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones in brain which can code for large proteins in vitro.
                                                                                                                                                                                                                                                                     ##cross-references EMBL:AB014534; NID:d1204289; PID:d1032570
                                                                                                                                                                                                   preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                        ##experimental_source brain
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Best Local Similarity 53.1%;
Matches 17; Conservative
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##residues 1-13
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ACCESSIONS
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                         REFERENCE
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      atrial natriuretic peptide receptor; atrionatriuretic peptide receptor A; guanylate cyclase A, membrane-bound guanylate cyclase (EC 4.6.1.2) A #formal_name Homo sapiens #common_name man 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Pardhasaradhi, K.; Kutty, R.K.; Gentleman, S.; Krishna, G. #journal Cell. Mol. Neurobiol. (1994) 14:1-7
#title Expression of mRNA for atrial natriuretic peptide receptor guanylate cyclase (ANPRA) in human retina.
#cross-references MUID:95042574
#accession 152846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *superfamily membrane-bound quanylate cyclase; guanylate cyclase catalytic domain homology; natriuretic peptide binding domain homology; protein kinase homology ATP: carbon-oxygen lyase; cGMP blosynthesis; glycoprotein; hormone receptor; phosphorus-oxygen lyase; transmembrane
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#domain transmembrane #status predicted #label TMM\
#domain intracellular #status predicted #label INT\
#domain protein kinase homology #label KIN\
#domain protein kinase catalytic domain homology
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predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain natriuretic peptide-binding domain homology
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#formal_name Homo sapiens #common_name man
01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change
                                                                                                                                                                                            Lowe, D.G.; Chang, M.S.; Hellmiss, R.; Chen, E.; Singh, Garbers, D.L.; Goeddel, D.V.
EMBO J. (1989) 8:1377-1384
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                                                                                                                                                                                                                                                          #title Human atrial natriuretic peptide receptor defines a paradigm for second messenger signal transduction. #cross-references MUID:89356605
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natriuretic peptide receptor A precursor - human
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##molecule_type mRNA
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##cross-references EMBL:X15357; NID:q28229; PID:g28230
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##cross-references GDB:125199; OMIM:108960
#map_position 1q21-1q22
CLASSIFICATION #sunamfa...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##rosidues 634-1048 ##label RES ##cross-references GB:S72628; NID:g619241 ##experimental_source retina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #type fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 LLLLLLPPLLLLLRGSHAGNL 35
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                                                                                                                                                     S04459; I52846
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                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 15; Conserv
                                                                                                                                                                         S04459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T00382
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                                                                                                                                                                                                                                                                                                                                                                                 ##residues
                  ALTERNATE_NAMES
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                                                                                                                                                                                                                                                                                                                                   #accession
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495-1061
526-808
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                                                                                                                                                                                                                                            #journal
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                                                                                                                                                                         REFERENCE
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                                                                CONTAINS
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                                                                                       ORGANISM
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                                                                                                           DATE
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#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeler, K.; Gas, S.; Barry III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Ollver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Taylor, K.; Whitehead, S.; Barrell, B.G. Taylor, M.; Moltehead, S.; Moltehead,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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##cross-references GB:295390; GB:AL123456; NID:g3261766; PID:e316057;
PID:g2104375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 FLAAADGANDASDHIQQMASACRATRLVLGGYSQGAAVIDIVTAAP-LPGL-GFTQPLPP 153
A70565 #type complete
probable cutinase precursor - Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.8%; Score 88; DB 2; Length 226; Best Local Similarity 28.6%; Pred. No. 3.46e+00; Matches 22; Conservative 20; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #length 226 #molecular-weight 23113
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                                                                                                                                (strain H37RV)
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Run on:

Fri Aug 20 21:18:21 1999; MasPar time 2.85 Seconds 437.587 Million cell updates/sec

Tabular output not generated.

>US-08-938-548B-10 (1-123) from US08938548B.pep 899 1 VPWAAVTLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

106580 seqs, 10152877 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Database:

Mean 27.574; Variance 124.910; scale 0.221 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	9.49e+00	1.32e+01	2.57e+01	2.57e+01	2.57e+01	2.57e+01	3.02e+01	3.02e+01	3.02e+01	3.02e+01	3.56e+01	3.56e+01	4.18e+01	4.18e+01	4.18e+01	4.18e+01	4.92e+01	4.92e+01	4.92e+01	4.92e+01	5.78e+01	5.78e+01	5.78e+01
	Description	Sequence 3, Applicatio	Sequence 4, Applicatio	2,	2,	7	'n	ý	9	9	2,	Patent No. 5175255.	Seguence 4, Applicatio	ř.	Patent No. 5175255.	Patent No. 5175255.	Sequence 1, Applicatio	Seguence 4, Applicatio	Sequence 4, Applicatio	Sequence 12, Applicati	Sequence 2, Applicatio	Sequence 4, Applicatio	Patent No. 5194596.	Sequence 9, Applicatio
SUMMAKLES	Q QI			US-08-299- S	,		US-08-026- S		US-08-243- S	PCT-US94-0 S	0	5175255-4 P	1				,	,	US-07-794- S	US-08-555- S	PCT-US95-0 S	US-08-387- S	5194596-15 P	PCT-US96-0 S
	DB	7	Н	Н	Н	Н	Н	7	Н	٣	m	4	7	4	4	4	Н	Н	Н	7	m	-	4	r
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	Score	90	88	84	84	84	84	83	83	83	83	82	82	81	81	81	81	80	80	80	80	79	79	79
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8.8 3170 2 US-07-642- Sequence 5, Applicatio 5.78e+018.8 4550 2 US-08-804- Sequence 4, Applicatio 5.78e+018.7 442 2 US-08-693- Sequence 2, Applicatio 6.78e+018.7 184 2 US-08-693- Sequence 2, Applicatio 6.78e+018.7 1184 1 US-08-446- Sequence 20, Applicati 6.78e+018.7 1184 2 US-08-965- Sequence 20, Applicati 6.78e+018.7 1184 1 US-08-966- Sequence 20, Applicati 6.78e+018.7 1187 1 US-08-97- Sequence 20, Applicati 6.78e+018.7 1187 1 US-08-97- Sequence 8, Applicati 6.78e+018.7 1187 3 US-08-97- Sequence 8, Applicati 6.78e+018.6 589 1 US-07-668- Sequence 2, Applicatio 7.96e+018.6 589 3 PCT-US95-1 Sequence 2, Applicatio 7.96e+018.6 613 2 US-08-429- Sequence 2, Applicatio 7.96e+018.6 613 2 US-08-455- Sequence 2, Applicatio 7.96e+018.6 613 3 PCT-US94-1 Sequence 2, Applicatio 7.96e+018.6 613 2 US-08-971- Sequence 2, Applicatio 7.96e+018.6 1865 2 US-08-971- Sequence 2, Applicatio 7.96e+018.6 2509 1 US-08-971- Sequence 2, Applicatio 7.96e+018.6 2509 1 US-08-971- Sequence 2, Applicatio 7.96e+018.5 2 US-08-971- Sequence 2, Applicatio 9.33e+018.5 2 US-08-971- Sequence 2, Applicatio 9.33e+018.5 231 3 PCT-US94-0 Sequence 2, Applicatio 9.33e+019.5 200-000000000	ALIGNMENTS 169A-3 STANDARD; PRT; 954 AA.	Sequence 3, Application US/08749169A Sequence 3, Application US/08749169A Patent No. 5846770 GENERAL INFORMATION: APPLICANT: LAVALLIE, Edward APPLICANT: LAVALLIE, Edward APPLICANT: LAVALLIE, Edward TITLE OF INVENTION: CHORDIN COMPOSITIONS NUMBER OF ESCHOENCES: ADDRESSEE: Genetics Institute, Inc. STREE: 87 CambridgePark Drive CITY: Cambridge CITY: Cambridge CITY: Cambridge CITY: STATE: Massachusetts COMUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMUTER: IBM PC COMPATIDE ORDERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UNMBER: US/08/749,169A FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: LAZAR, Steven R. REGISTRATION SYSTEM: (617) 498-8260 TELECOMMUNICATION INFORMATION: TELEPONAR: (617) 498-8260 TELECOMMUNICATION INFORMATICS: LENGTH: 954 amino acids TYPORMATION CON SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 954 amino acids TOPOLOGY: linear MOLECULE TYPE: Protein
887777777777799999999	-169A-3	3, Applica 3, Applica 5, 5846770 INFORMATI ANT: RACANT: LAV ANT: DER OF INVENT OF SEQUED SPONDENCE SPONDENCE SPESSES 10 CAMPLICA 10 CAMPLICA 11 CATION N 12 APPLICA 12 CATION N 13 APPLICA 14 APPLICA 15 APPLICA 16 CAMPLICA 17 APPLICA 18 APPLICA 19 APPLICA 18 APPLICA 18 APPLICA 19 APPLICA 10 APPLICA 11 APPLICA
5 5 5 6 6 7 7 7 7 7 7 8 8 8 7 7 7 7 7 8 8 8 7 7 7 7 7 8 8 8 7 7 7 7 7 8 8 8 7 7 7 7 7 7 8 8 8 7 7 7 7 7 7 7 8 8 8 7 7 7 7 7 7 7 7 7 8 8 8 7 7 7 7 7 7 7 7 7 7 7 8 8 8 7	1 5-08-74 «XXXX	Sequence 3, App Sequence 3, App Patent No. 584 GENERAL INFOR APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF IN UNMERS OF SORRESPONDE ADDRESSED STRATE: COMPUTER: COMPUTER: OPERATION PR MEDIUM TY COMPUTER: OPERATION PAPP APPLICANT FILLED HONE TELECHONNE TOPOLOGY: TYPE: ANDICHOLOGY: TYPE: AN
33353335555555555555555555555555555555	RESUL: ID (XX XX AC XX DT	# × × × × × × × × × × × × × × × × × × ×

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Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: Masayoshi MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nishiohata Residence 1-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.3%; Score 84; DB 1; Length 238; 8.4%; Pred. No. 2.57e+01; tive 2; Mismatches 3; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
                                                                                                                                                                                                                    OPERATING SYSTEM: Apple System 7.1 SOFTWARE: Microsoft Word for Apple, Version 5.1a CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/240,124
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STREET: 5214, Nishiohata-machi
CITY: Nijaata-shi
STATE: Nijaata ken
COUNTRY: JAPAN
                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TORRAATION:
TELEFAN: (206) 587-0430
TELEFAN: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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JENCE 238 AA; 26350 MW; 315668 CN;
       ADDRESSEE: IMMUNEX CORPORATION STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08026138E
                                                                                                                      ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 238 amino acids
amino acid
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Best Local Similarity 68.4%;
Matches 13; Conservative
                                                   CITY: SEATTLE
STATE: WASHINGTON
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                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Patent No. 5516658
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETIT, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SOUGHENCES: 4
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
NUMBER OF SEQUENCES:
A CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATILE
STATE: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
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                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintoon
COMPUTER: Apple Macintoon
COPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30 MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 AA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MX-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
RECISTRATION NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 238 AA; 26350 MW; 315668 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Sequence 2, Application US/08240124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (200,
TELEFAX: (200,
TELEFAX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAAPLILLLLLLVPVPLLPL 20
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Best Local Similarity 68.4%;
Matches 13; Conservative
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Sequence 2, Application PC/TUS9106532
GENERAL INFORMATION:
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses
TITLE OF INVENTION: Vaccines and Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
9.2%; Score 83; DB 3; Length 235;
Best Local Similarity 55.6%; Pred. No. 3.02e+01;
Matches 10; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two First National Plaza Suite 2100 CITY: Chicago STATE: Illinois COUNTRY: USA
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION: May 11, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/11,758
FILING DATE: AUGUST 25, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: AUGUST 12, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: MAY 24, 1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: MAY 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE 235 AA; 26415 MW; 293990 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9106532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
NAME: MALSKA, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 283-0644
TELER: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 235 amino acids
amino acid
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2 PWAAVT-LLLLLLEPPAL 18
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PCT-US91-06532-2
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GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Lyman, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES:
RODRESSE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seatle ADDRESS:
ADDRESSE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seatle Mashington
COMPUTER: Washington
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.2%; Score 83; DB 1; Length 235; Best Local Similarity 55.6%; Pred. No. 3.02e+01; Matches 10; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 AA
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAX-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: AUGUST 25, 1993
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEX: 756825
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: MAY 24, 1993
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 235 AA; 26415 MW; 293990 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application PC/TUS9405365
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TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Thomason, Arlen R.;Nicholson, Margery
TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.0%; Score 81; DB 4; Lo
Best Local Similarity 46.9%; Pred. No. 4.18e+01;
Matches 15; Conservative 9; Mismatches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.0%; Score 81; DB 4; L. Local Similarity 46.9%; Pred. No. 4.18e+01; hes 15; Conservative 9; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 LORLLQGDSGKEDGAELDLNMTRSHSGGELES 75
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                      245 AA; 27563 MW; 324570 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 241
4CE 261 AA; 29326 MW; 367179 CN;
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APPLICATION NUMBER: 941,970
FILING DATE: 15-DEC-1986
APPLICATION NUMBER: 896,485
FILING DATE: 3-AUG-1986
APPLICATION NUMBER: 705,175
FILING DATE: 25-FEB-1985
APPLICATION NUMBER: 660,496
FILING DATE: 12-OCT-1984
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                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 226
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5175255-8
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5175255-2
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Matches
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Sat Aug 21 11:58:41 1999

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 5.77 Seconds 602.480 Million cell updates/sec Fri Aug 20 21:16:51 1999; Run on:

Tabular output not generated.

>US-08-938-548B-10 (1-123) from USO8938548B.pep 899 1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123 Description: Perfect Score:

Scoring table:

Sequence:

PAM 150 Gap 11

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Statistics:

1:swissprot

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.468; Variance 75.472; scale 0.549

SUMMARIES

		dЮ			SUPPRINCES			
Result No.	Score	Query	Length	DB	Ð	Description	Pred. No.	
н	103	11.5		П	GPV_RAT	<u>ы</u>	8.73e-03	
8		11.2	131	Н	SECR_PIG	SECRETIN PRECURSOR (FR	1.73e-02	
m	٥	10.7		-4	FBLA_HUMAN	FIBULIN-1, ISOFORM A P	9.21e-02	
4	96	10.7	601	Н	FBLB_HUMAN	FIBULIN-1, ISOFORM B P	9.21e-02	
Ŋ	96	10.7	683	Н	FBLC_HUMAN	FIBULIN-1, ISOFORM C P	9.21e-02	
9	96	10.7	703	-	FBLD_HUMAN	FIBULIN-1, ISOFORM D P	9.21e-02	
7	91	10.1	440	Н	LCAT_HUMAN	PHOSPHATIDYLCHOLINE-ST	4.64e-01	
ω	88	6.6	602	Н	PGH1_RAT	PROSTAGLANDIN G/H SYNT	8.72e-01	
σ		9.9	1001	Н	ANPA_HUMAN	ATRIAL NATRIURETIC PEP	8.72e-01	
10			254	۲	41BL_HUMAN	4-1BB LIGAND (4-1BBL).	1.19e+00	
11	88	ø.	438	Н	LCAT_MOUSE	PHOSPHATIDYLCHOLINE-ST	1.19e+00	
12			322	Н	RLUC_HAEIN	RIBOSOMAL LARGE SUBUNI	2.20e+00	
13			440	Н	LCAT_PAPAN	PHOSPHATIDYLCHOLINE-ST	2.20e+00	
14	98	9.6	497	٦	SC14_YARLI	SEC14 CYTOSOLIC FACTOR	2.20e+00	
15	98		1663	7	CO3_RAT	COMPLEMENT C3 PRECURSO	2.20e+00	
16	85	9.5	236	П	PLC1_BOVIN	PLACENTAL LACTOGEN I P	2.98e+00	
17	85		317	П	LIP1_PSYIM	LIPASE 1 PRECURSOR (EC	2.98e+00	
18	85	9.5	334	-	FEPD_ECOLI	FERRIC ENTEROBACTIN TR	2.98e+00	
19	85		1027	П	CAFF_RIFPA	FIBRIL-FORMING COLLAGE	2.98e+00	
20	84	9.3	90	П	VGE_BPPHX	LYSIS PROTEIN (E PROTE	4.03e+00	
21	84	9.3	06	-	VGE_BPS13	LYSIS PROTEIN (E PROTE	4.03e+00	
22	84	9.3	238	Н	EFA3_HUMAN	EPHRIN-A3 PRECURSOR (E	4.03e+00	
23	84	9.3	251	П	C1QB_HUMAN	COMPLEMENT C10 SUBCOMP	4.03e+00	

1 LIP3_MORSP 1 RLUC_ECOLI 1 RV_DROME 1 LSHR_PIG 1 PTPX_MOUSE 1 TALI_MOUSE 1 GPBB PAPCY		
84 9.3 319 1 RLUC_ECOLI 84 9.3 384 1 RN_DROME 84 9.3 696 1 LSHR_PIG 84 9.3 1001 1 PTPX_MOUSE 84 9.3 2541 1 TALI_MOUSE 83 9.2 208 1 GPBB PAPCY	IPASE 3 PRECURSOR (EC	4.03e+00
84 9.3 384 1 RN_DROME 84 9.3 696 1 LSHR_PIG 84 9.3 1001 1 PTPX_MOUSE 84 9.3 2541 1 TALL_MOUSE 83 9.2 208 1 GPBB PAPOY	IBOSOMAL LARGE SUBUNI	4.03e+00
84 9.3 696 1 LSHR_PIG 84 9.3 1001 1 PTPX_MOUSE 84 9.3 2541 1 TALL_MOUSE 83 9.2 208 1 GPBB PAPCY	GTPASE ACTIVATING PROT	4.03e+00
84 9.3 1001 1 PTPX_MOUSE 84 9.3 2541 1 TALI_MOUSE 83 9.2 208 1 GPBB PAPCY	LUTROPIN-CHORIOGONADOT	4.03e+00
84 9.3 2541 1 TALI_MOUSE 93 9.2 208 1 GPBB_PAPCY	PROTEIN-TYROSINE PHOSP	4.03e+00
83 9.2 208 1 GPBB PAPCY	ALIN.	4.03e+00
	PLATELET GLYCOPROTEIN	5.43e+00
83 9.2 224 1 OXO2_HORVU	OXALATE OXIDASE PRECUR	5.43e+00
83 9.2 235 1 FL3L_HUMAN SL	IL CYTOKINE PRECURSOR	5.43e+00
83 9.2 248 1 ICP3_HSV11	INFECTED CELL PROTEIN	5.43e+00
83 9.2 252 1 ICP3_HSV1D INFECTED	NFECTED CELL PROTEIN	5.43e+00
83 9.2 263 1 ICP3_HSV1F	INFECTED CELL PROTEIN	7
83 9.2 440 1 LCAT_RABIT	PHOSPHATIDYLCHOLINE-ST	5.43e+00
83 9.2 440 1 LCAT_RAT	PHOSPHATIDYLCHOLINE-ST	7
83 9.2 536 1 YABK_ECOLI	HYPOTHETICAL 59.6 KD P	5.43e+00
83 9.2 615 1 ALBU_CHICK	SERUM ALBUMIN PRECURSO	5.43e + 00
83 9.2 628 1 FTSH PORPU	CELL DIVISION PROTEIN	5.43e+00
83 9.2 676 1 ICPO_HSVBK	TRANS-ACTING TRANSCRIP	5.43e+00
83 9.2 676 1 ICPO_HSVBJ	TRANS-ACTING TRANSCRIP	4
83 9.2 1004 1 PTPX_RAT	PROTEIN-TYROSINE PHOSP	4.
83 9.2 1109 1 CYGD_CANFA RETINAL GUANYLYL	RETINAL GUANYLYL CYCLA	5.43e+00
83 9.2 1310 1 ACE_RABIT	ANGIOTENSIN-CONVERTING	5.43e+00
ALIGNMENTS		
SULT 1		
ID GFV_KAI STANDAKD; FKT; 36/ AA. AC 008770:		
15-JUL-1998 (REL. 36,	(TE)	
(REL. 36,	DATE)	
	(CD42D).	
VEGICUS (RAT).		
BONARIOIA; MEIAZOA; CHOKDAIA; VEKIEBKAIA; MAMMALIA; RODENTIA: SCIUROGNATHI: MURIDAE: MIRINAE: RATTUS		
[1]		
RP SEQUENCE FROM N.A.		

STRAIN-WIGTAR; TISSUE-LIVER;

X MEDLINE; 97275136.

A RAVANAT C., MORALES M., AZORSA D.O., MOOG S., SCHUHLER S.,
RAVANAT C., MORALES M., AZORSA D.O., MOOG S., SCHUHLER S.,
GENE Cloning of rat and mouse platelet glycoprotein V:
"Gene cloning of rat and mouse platelet glycoprotein V:
"Gene cloning of megakaryocyte-specific promoters and demonstration of functional thrombin cleavage.";

T identification of megakaryocyte-specific promoters and demonstration of functional thrombin cleavage.";

BLOOD 89:3253-3262(1997).

-I- FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND FACTOR-DEFENDENT PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A CRITICAL INTIMATING EVENT IN HEWOSTASIS (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SUBLICARITY: THE REPEARTED LEGCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 15.

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EMBL; 269594; E222201; -.
EMBL; 269594; E222201; -.
PLATELET; TRANSMEMBRANE; GLXCOPROTEIN; BLOOD COAGULATION;
PLATELET; TRANSMEMBRANE; GLXCOPROTEIN; SIGNAL.
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POTENTIAL. PLATELET GLYCOPROTEIN V. EXTRACELLULAR (POTENTIAL). POTENTIAL. 16 567 522 543 567 DOMAIN TRANSMEM DOMAIN

CYTOPLASMIC (POTENTIAL).

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ARGRAVES W.S., TRAN H., BURGESS W.H., DICKERSON K.; "Fibulin is an extracellular matrix and plasma glycoprotein with
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ARGRAVES W.S., DICKERSON K., BURGESS W.H., RUOSLAHTI E.;
"Fibulin, a novel protein that interacts with the fibronectin receptor beta subunit cytoplasmic domain.";
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PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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. 8; Indels
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A2D23E14 CRC32;
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01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
10-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBULIN-1, ISOFORM B PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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Pred. No.
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J. CELL BIOL. 111:3155-3164(1990).
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Best Local Similarity 57.1%;
Matches 16; Conservative
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   HOMO SAPIENS (HUMAN)
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41
566 AA;
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
ARGEAVES 91100426.
ARGEAVES W.S., TRAN H., BURGESS W.H., DICKERSON K.;
"Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure.";
                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 2, CALCIUM-BIN
EGF-LIKE 3, CALCIUM-BIN
EGF-LIKE 5, CALCIUM-BIN
EGF-LIKE 6, CALCIUM-BIN
EGF-LIKE 6, CALCIUM-BIN
EGF-LIKE 7, CALCIUM-BIN
EGF-LIKE 7, CALCIUM-BIN
EGF-LIKE 9, CALCIUM-BIN
EGF-LIKE 9, CALCIUM-BIN
EGF-LIKE 9, CALCIUM-BIN
EGF-LIKE 9, CALCIUM-BIN
                                                                                                          01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
101-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBULIN-1, ISOFORM A PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010; ASX_HYDROXYL; 4.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01086; EGF_2; 5.
HSSP; P35555; 1EMO.
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TLLLLLLLPPALLSLGVDAQPLP 29
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                                                                         STANDARD;
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PIR; A36346; A36346.
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                                                     JT 3
FBLA_HUMAN
P23142;
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SUBMITTED (SEP-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (SEP-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (SEP-1993) TO EMBL/GENBANK MATRIX.
SUBGELLGUAR LOCATION: EXTRACELLULAR MATRIX.
ALTERNATIVE PRODUCTS: FOUR FORMS OF FIBULIN-1; A (AC P23142), B (AC P23143), C (AC P23144) AND D (SHOWN HERE); DIFFERING ONLY IT THEIR C-TERMINAL REGIONS, ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS. SIGNAL; ALTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX; REPEAT; PLASMA; EGF-LIKE DOMAIN; CALCIUM-BINDING.

1 29 HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO. EGF-LIKE 1.
EGF-LIKE 2. CALCIUM-BINDING (PEGF-LIKE 3. CALCIUM-BINDING (PEGF-LIKE 4. CALCIUM-BINDING (PEGF-LIKE 5. CALCIUM-BINDING (PEGF-LIKE 6. CALCIUM-BINDING (PEGF-LIKE 9. SIMILARITY.

BY SIMILARITY. FIBULIN-1, ISOFORM D.
3 X AMAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3. 7029 17029 17029 17029 17039 1 DISULFID DISULFID DISULFID

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                JQ0036; JQ0036.
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205
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337
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                                                                                                                                                    POLYMORPHISM;
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                                                                                                                                                                                                                               ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUM. MUTATY 8:79-82(1996).

-!- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIES THE FREE CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.

-!- CATALYTIC ACTIVITY: PHOSPHATIDYCHOLINE + STEROL = STEROL ESTERR + 1-ACYLGLYCEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CAN BE TRANSFERED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
                                                                                                                                                                                                                                                                                                                                                                   of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Deficiency of lecithin: cholesterol acyltransferase due to compound heterozygosity of two novel mutations (Gly33Arg and 30 bp ins) in the
                                                                                                              "Genetic and phenotypic heterogeneity in familial lecithin:
cholesterol acyltransferase (LCAT) deficiency. Six newly identified
defective alleles further contribute to the structural heterogeneity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A single G to A nucleotide transition in exon IV of the lecithin: cholesterol acyltransferase (LCAT) gene results in an Arg140 to His substitution and causes LCAT-deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNKE H., ASSMANN G.; "Complete deficiency of plasma lecithin-cholesterol acyltransferase (LCAT) activity due to a novel homozygous mutation (Gly-30-Ser) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT HIS-164.
BEDLINE; 95331753.
STERRER E., HAUBENWALLNER S., HOERL G., GIESSAUF W., KOSTNER G.M.,
ZECHNER R.;
FUNKE H., VON ECKARDSTEIN A., PRITCHARD P.H., HORNBY A.E., WIEBUSCH H., MOTTI C., HAYDEN M.R., DACHET C., JACOTOT B., GERDES FAERGEMAN O., ALBERS J.J., COLLEONI N., CATAPANO A., FROHLICH J., ASSMANN G.;
                                                                                                                                                                                                                                                                                                                               HILL J.S., O K., WANG X., PRITCHARD P.H.;
Lecithin:cholesterol acyltransferase deficiency: identification
causative gene mutation and a co-inherited protein polymorphism."
BIOCHIM. BIOPHYS. ACTA 1181:321-323(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95227171.
WIEBUSCH H., CULLEN P., OWEN J.S., COLLINS D., SHARP P.S., FUNKE
ASSMANN G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THIS ENZYME.
DISEASE: DEFECTS IN LCAT ARE THE CAUSE OF NORUM AND FISH EYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 96400966.
OWEN J.S., WIEBUSCH H., CULLEN P., WATTS G.F., LIMA V.L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS. ARG-57 AND 10 AA INSERTION IN POSITION 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; XU6537; -; NOT_ANNOTATED_CDS.
EMBL; X04681; G187025; -.
EMBL; X04981; G34287; -.
EMBL; M17959; G386858; -.
                                                                                                                                                                                              in this disease.";
J. CLIN. INVEST. 91:677-683(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.";
MOL. GENET. 4:143-145(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENET. 96:105-109(1995).
                                                                                                                                                                                                                                                                              VARIANTS THR-117 AND CYS-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M12625; G307117; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT AS ACCEPTOR
                                                                                                                                                                                                                                                                                                         MEDLINE; 93305754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT SER-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCAT gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASES.
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the

PIR; A00571; XXHUN. PIR; A29661; A29661 PIR; A25575; A25575

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGH1_RAT STANDARD; PRT; 602 AA.

063921; 062731; 063684;

15-DEC-1998 (REL. 37, CREATED)

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -1) (COX-1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1) (PROSTAGLANDIN H2

SYNTHASE 1) (PGH SYNTHASE 1) (PGHS-1) (PHS 1).

PTGS1 OR COX1 OR COX-1.

RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNTT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE.
-!- THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE.
-!- THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS
MIM; 245900; -.
PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) = PROSTAGLANDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KITZLER J., HILL E., HARDMAN R., REDDY N., PHILDOT R., ELING T.E.;
"Analysis and quantitation of splicing variants of the TPA-inducible
PGHS-1 mRNa in rat tracheal epithelial cells.";
ARCHE BIOCHEM BIOPHYS. 316:856-863 [1995].
- PUNCTION: MYY PLAY AN IMPORTANT ROLE IN REGULATING OR PROMOTING
CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E., WILSON C.B., HWANG D., "Cloning two isoforms of rat cyclooxygenase: differential regulation of their expression.";
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                         LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H2 + A + H(2)O.
-!- PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHÓRDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                       Score 91; DB 1; Length 440;
Pred. No. 4.64e-01;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARCH. BIOCHEM. BIOPHYS. 307:361-368(1993)
                                                                                                                                                                                                                                                                                    omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-FISHER 344; TISSUE-TRACHEA; MEDLINE; 95168876.
                                                                   DISEASE MUTATION.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                 of annotations
                                                                                                                                                                                                                                                                                                                                                                                                            7 PWQWVTLLLGLLLPPA 22
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C68C1B27 CRC32;

26624 MW;

254 AA;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOPROTEIN; SIGNAL-ANCHOR.

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUR. J. IMMUNOL. 24:2219-2227(1994).
-!- FUNCTION: INDUCES THE PROLIFERATION OF ACTIVATED PERIPHERAL BLOOD
I CELLS. MAY HAVE A ROLE IN ACTIVATION-INDUCED CELL DEATH (AICD).
MAY PLAY A ROLE IN COGNATE INTERACTIONS BETWEEN I CELLS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 94374434.
ALDERSON M.R., SMITH C.A., TOUGH T.W., DAVIS-SMITH T., ARMITAGE R.J., FALER B., ROUX E., BAKER E., SUTHERLAND G.R., DIN W.S., GOODWIN R.G.; "Molecular and biological characterization of human 4-1BB and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B CELLS/MACROPHAGES.
SUBUNIT: HOWOTRIMER (POTENTIAL)
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENIA, LUNG, SKELETAL
MUSCLE AND KIDNEY.
                                                                                                                                                                                                                                                                  Gaps
            NATRIURETIC PEPTIDE RECEPTOR A.
                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                        Score 89; DB 1; Length 1061;
Pred. No. 8.72e-01;
0; Mismatches 6; Indels
                    EXTRACELLULAR (POTENTIAL).
                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                 INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
POTENTIAL.
                                                           PROTEIN KINASE LIKE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                C6117B45 CRC32;
                                                                                                                                                                                                                                                                                                                                                                41BL_HUMAN STANDARD; PRT; 254 AA. P41273; 01-FEB-1995 (REL. 31, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) 4-1BB LIGAND (4-1BBL).
                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                         9.98;
                                                                                                                                                                                                                                                  68.2%;
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1061 AA;
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les 15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MERONI G., MALGARETTI N., MAGNAGHI P., TARAMELLI R.;
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
ILPOPROTEINS: AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE CHOLESTEROL TRANSFORTED IN PLASMA LIPOPROTEINS.
CATALYTIC ACTIVITY: PROSPHATIDYLCHOLINE + STEROL ESTER +
1-ACYLGINCEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CAN BE TRANSFERRED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Tissue-specific expression, developmental regulation, and chromosomal mapping of the lecithin: cholesterol acyltransferase gene. Evidence for expression in brain and testes as well as liver."; J. BIOL. CHEM. 264:21573-21581(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A34188; XXMSN.
MGD; MGI:96755; LCAT.
PROSITE; PS00120; LIPASE_SER; 1.
PROSITE; PS00120; LIPASE_SER; 1.
SIGNAL.
1 24
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT AS ACCEPTOR).
ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THIS ENZYME.
-!- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
                                                                                                                                                                                                01-AGG-1990 (REL. 15, CREATED)
01-AGG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-AGV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 90094326.
WARDEN C.H., LANGNER C.A., GORDON J.I., TAYLOR B.A., MCLEAN J.W.,
                                    1;
                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
   Length 254;
Score 88; DB 1; Length 254;
Pred. No. 1.19e+00;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                       438 AA
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BY SIMILARITY.
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                                                                                                                                                                       PRT;
 Query Match 9.8%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                   27 LPWALVAGLLLLLLLAAA 44
                                                                                      1 VPWAAVT-LLLLLLLPPA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J05154; G293697; -. EMBL; X54095; G52874; -.
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     ACYLTRANSFERASE).
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205
74
337
                                                                                                                                                                   LCAT_MOUSE P16301;
                                                                                                                                                                                                                                                                                                                                                                                                                                           LUSIS A.J.;
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SUNDSTROM S.A., KOMM B.S., PONCE-DE-LEON H., YI Z., TEUSCHER C.,
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                        LYTTLE C.R.;
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PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                   SEQUENCE FROM N.A.

C STRAIN-ATC 20460 / W29;

MEDLINE; 9418653:

A LOPEZ M.C., NICAUD J.-M., SKINNER H.B., VERGNOLLE C., KADER J.-C.,

A BANKAITIS V., GALLLARDIN C.;

"A phosphatidylinositol/phosphatidylcholine transfer protein is

required for differentiation of the dimorphic yeast Yairowia

I ipolytica from the yeast to the mycelial form.";

J. CELL BIOL. 124.113.127(1994).

C. I- FUNCTION: REQUIRED FOR TRANSPORT OF SECRETORY PROTEINS FROM THE

GOLGI COMPLEX. CATALYZES THE TRANSFER OF PHOSPHATIDYLINOSITOL AND

PHOSPHATIDYLCHOLINE BETWEEN MEMBRANES IN VITRO.

C. I- SUBCELLULAR LOCATION: ASSOCIATED WITH THE GOLGI COMPLEX AS A

PERIPHERAL MEMBRANE PROTEIN (BY SIMILARITY).

C. I- SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.
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STRAIN=WISTAR; TISSUE-LIVER;
MEDLINE; 90.245672.
MISUMI Y., SOHDA M., IKEHARA Y.;
"Nucleotide and deduced amino acid sequence of rat complement C3.";
NUCLEIC ACIDS RES. 18:2178-2178(1990).
  FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 79062262.
JACOBS J.W., RUBIN J.S., HUGLI T.E., BOGARDI R.A., MARIZ I.K.,
DANIELS J.S., DAUGHADAY W.H., BRADSHAW R.A.;
"Purification, characterization, and amino acid sequence of ra
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 497;
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01-AGG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86; DB 1; Leng
Pred. No. 2.20e+00;
9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 AVLLLLELLLPSRLLLPRLLLPRRQGSRSRCCQDRHCPC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6209E8FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1663 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSPORT; PROTEIN TRANSPORT; GOLGI STACK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO-RICH.
LEU-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anaphylatoxin (C3a).";
BIOCHEMISTRY 17:5031-5038(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1316-1595 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L20972; G311167; -. PFAM; PF00650; CRAL_TRIO; 1. HSSP; P24280; 1AUA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                  DIPODASCACEAE; YARROWIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 671-748.
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EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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CO3_RAT
P01026;
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"Estrogen regulation of tissue-specific expression of complement C3."; J. BADL. CHEM. 264.16947 (1989).
-!- FUNCTION: C3 PLAYS A CENTRAL ROLL IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL
                                                               COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CBLL SHERACE CARBOHYDRATES OR IMMUNE AGGREGATES. FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3, C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDICES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
                                                                                                                                                                                                                                                                         SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG RESIDUES. FORMING TWO CHAINS, BETA 6 ALPHA, LINKED BY A DISULFIDE BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN, RELEASING C3A ANAPHYLACTOXIN 6 GENERATING C3B (BETA CHAIN + ALPHA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENT PATHWAY; COMPLEMENT ALTERNATE PATHWAY; PLASMA; INFLAMMATORY RESPONSE; GLYCOPROTEIN; SIGNAL.

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                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
-!- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
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MW; 0428CF63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86; DB 1; L. Pred. No. 2.20e+00; 5; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52477; G56954; -.
EMBL; M20866; G554423; ALT_SEQ.
PIR; A01260; A01260.
PIR; S15764; S15764.
PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
PROSITE; PS01179; ANAPHYLATOXIN_2; 1.
PROMY: PF00207; A2M; 1.
HSSP; P01024; 1C3D.
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Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Aug 20 21:17:24 1999; MasPar time 11.47 Seconds 585.113 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-938-548B-10 (1-123) from USO8938548B.pep 899 1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mmmal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 39.662; Variance 86.129; scale 0.460 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	6.00e-145	3.85e-136	1.82e-113	2.23e-111	3.75e-03	3.22e-02	3.44e-01	6.13e-01	1.08e+00	1.44e+00	1.44e + 00	1.90e+00	1.90e+00	3.32e+00	3.32e+00	4.36e+00	5.73e+00	5.73e+00	7.52e+00	7.52e+00
Description	HYPOCRETIN (PREPRO-ORE	PREPRO-OREXIN.	PREPRO-OREXIN.	PREPRO-OREXIN PRECURSO	GDNF FAMILY RECEPTOR A	HYPOTHETICAL 74.6 KD P	FRIZZLED PROTEIN HOMOL	FRIZZLED-1.	ACYLOXYACYL HYDROLASE.	LEUCINE ZIPPER WITH BA	TIGHT JUNCTION PROTEIN	PROLINE- AND LEUCINE-R	PAIRED BOX PROTEIN PAX	L-1 METALLO-BETA-LACTA	SORTILIN PRECURSOR.	KIAA0634 PROTEIN (FRAG	HYPOTHETICAL 23.1 KD P	THYROID HORMONE INDUCE	HYPOTHETICAL 25.9 KD P	PUTATIVE GPI-ANCHORED
Ü	055241	055232	043612	077668	609090	023352	008463	070421	035298	091640	095168	041051	018381	051899	099523	075129	006319	091654	005582	076660
DB	11	11	4	9	4	10	Π	11	디	13		10	Ŋ	~	4	4	7	13	~	Ŋ
% Query Match Length	130	130	131	131	400	619	641	626	574	331	1174	106	857	290	833	1321	226	335	252	396
% Query Match	100.0	94.9	81.6	80.4	12.6	11.8	10.9	10.7	10.5	10.3	10.3	10.2	10.2	10.0	10.0	6.6	9 8	9.8	9.7	9.7
Score	899	853	734	723	113	106	96	96	94	93	93	92	92	06	06	83	88	88	87	87
Result No.		7	3	4	2	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20

7.	9.83e+00	9.83e+00	- 9.83e+00	9.83e+00	H	7 1.28e+01	4	. 1.67e+01	? 1.67e+01	9 1.67e+01	9 1.67e+01	7 1.67e+01	1.67e+01	1.67e+01	2.17e+01	. 2.17e+01	. 2.17e+01	(2.17e+01	4 2.17e+01	A 2.17e+01	2.17e+01	Α.	2.82e+01
SIMILARITY TO MOUSE SM	HYPOTHETICAL 34.4 KD I	HYPOTHETICAL 48.1 KD 1	LEUCINE-RICH RECEPTOR	NB-2.	PORCINE MEMBRANE COFAC	RNA-DEPENDENT RNA POLI	ANION EXCHANGER ISOFOR	108 PROTEIN PRECURSOR	HYPOTHETICAL 30.9 KD I	HYPOTHETICAL 33.3 KD 1	HYPOTHETICAL 72.6 KD I	ANION EXCHANGER 2 A (I	R32184_2.	DIACYLGLYCEROL KINASE	3' ORF.	NEUROVIRULENCE FACTOR	MYOMODULIN (FRAGMENT)	MYOMODULIN PRECURSOR	LECITHIN: CHOLESTEROL 1	MALTASE-LIKE PROTEIN A	PCBR.	MHC CLASS I HEAVY CHA	VERY LARGE TEGUMENT PR
018780	085011	P72841	082432	P97527	002839	083101	060471	043495	033285	069681	065568	060470	060391	000542	061639	012396	027916	007974	035849	017021	P72405	046723	P89459
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22	23	24	52	26	27	28	58	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45
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MEDLER E., MANGTOT I., BENT E., LOVE K., GOODMAN H., DEAN C.,

MEDLEY P., HUDSON S.A., PATEL K., MURCHY G., PIFFANELLI P., WEDLER H.,

MEDLER E., WAMBUTT R., WEITZENEGGER T., POUL T.M., TERRYN N.,

AGIELEN J., VILLARROEL R., DE CLERCK R., VAN MONTAGU M., LECHARNY A.,

ANDORG S., GY I., KREIS M., LAO N., KNYANAGH T., HEMPEL S., KOTTER P.,

BYLYEY M., JAMES R., MONTFORT A., PONS A., PUIGDOMENECH P., DOUKA A.,

VOUKELATOU E., MILIONI D., HATZOPOULOS P., PIRAVANDI E., OBERMAIER B.,

HILBERT H., DUESTERHOFT A., MOORES V., ECOKE R., BENGER C.,

ANDELSENY M., VOET M., VOLCKAERI G., MEWES H.W., KLOSTERMAN S.,

ANDELSENY M., VOET M., VOLCKAERI G., MEWES H.W., KLOSTERMAN S.,
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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ARABIDDPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTLES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                   68 KRRPGPPGLQGRLQRLLQASGNHAAGILTMGRRAGAEPAPRLCPGRRCLAAAASSVAPGG 127
                                                                                            8 VSWATVTLLLLLLLLLLPPAVLSPGAAAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLG 67
   Gaps
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EMBL, AF651767; G2961532; -. SEQUENCE 400 AA: 44538 MW; 6DFB5381 CRC32;
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      Indels
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EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
RECEPTOR ALPHA 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             023352;
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
   Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.75e-03;
atches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PWAAVTLLLLLLPPPALLSLGVDAQPLPDCCRQKTCSC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       679 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.6%; Score 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 47.4%; Pred. No.
Matches 18; Conservative 9; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TREMBLREL. 07, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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13;
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            128 RSGI 131
                                                                                                                                                                                                                                                                                                                                                                         120 GSGV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (
01-AUG-1998 (
01-AUG-1998 (
GDNF FAMILY F
66
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060609
060609;
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023352
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   Matches
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DO 02

DO 02

DO 01

DO 01
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=SPRAGUE-DAWLEY; TISSUE-OSTEOSARCOMA;

KARDLINE; 93094228.

CHAN S.D.H., KARPE D.B., FOWLKES M.E., HOOKS M., BRADLEY M.S.,

VUONG V., BAMBINO T., LIU M.Y.C., ARNAUD C.D., STREWLER G.J.,

NISSENSON R.A.;

"Two homologs of the Drosophila polarity gene frizzled (fz) are

widely expressed in mammalian tissues.";

J. BIOL. CHEM. 267:25202-25207(1992).

-!- FUNCITON: MAY BE INVOLVED IN TRANSDUCTION AND INTERCELLULAR

TRANSMISSION OF POLARITY INFORMATION DURING TISSUE MORPHOGENESIS

AND/OR IN DIFFERENTIATED TISSUES.

-!- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY, LIVER, UTERUS, OVARY

AND HEART. LOWER LEVELS SEEN IN BRAIN AND INTESTINE.

EXTREMELY LOWER LEVELS SEEN IN BRAIN AND INTESTINE.

C.!- DEVELOPMENTAL STRAE: EXPRESSED PREDOMINANTLY IN NEONATAL TISSUES,

AT LOWER LEVELS IN ADULT.
                                                                                                                                                                                                                                                              4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHÓRDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                          598 KYCRSK-YETIHGONHDNAADVLELAIKREMPAELL-R-ASLRHTNEDQRNFLLNVGRSA 654
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                              Gaps
                               of
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SCHUELLER C., CHALWATZIS N.;
"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 Arabidopsis thaliana";
NATURE 391:485-488(1998).
                                                                                                                                                                                                         Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 98; DB 11; Length 641;
                                                                                                                                                                                                       Score 106; DB 10; Length 67
Pred. No. 3.22e-02;
16; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.44e-01;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MEMBL; L0229; G310117; -. DEVELOPMENTAL PROTEIN; TRANSMEMBRANE; GLYCOPROTEIN. DOMAIN 72 312 EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
EA083C54 CRC32;
                                                                                                                                                          B301B713 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRIZZLED PROTEIN HOMOLOG 1 (FZ-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 WARGLLLLLWLLEAPLL-LGVRAQP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WAAVILLILLILPPALLSLGVDAQP 27
                                                                                                                                                        679 AA; 74635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71027 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01,
                                                                                                                                                                                                    y Match
Local Similarity 32.3%;
hes 20; Conservative
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Best Local Similarity 64.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                EMBL; Z97337; E326841; -. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641 AA;
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Search completed: Fri Aug 20 21:18:03 1999
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                                                                                                                                                                                                                                                                              RESULT 14
1D 051899
DT 01-UUN-1
DT 01-UUN-1
DE L-1 METAS
GN BLAS.
GS STENOTRO
OC SANTHOMO
OC XANTHOMO
OC XANTHOMO
OC XANTHOMO
N.RN [1]
N.RN [1]
N.RN SEQUENCE
RC STRAIN=G
RA SANGCHAG
RA S
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Q99523
Q99523;
                                                    200
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LARVAL, ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN
LARVAL, ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN
LARVAL ST THAT OF THE LARVAL ISOFORM.

-1- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.

C -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.

REMBL; X79492; E354266; --

REMBL; X79492; E354266; --

REMBL; X79492; E354266; --

REMBL; X79492; E355426; --

REMBL; X79492; E355421; HOMEOBOX_2; 1.

REMBL; X79492; E356071; HOMEOBOX_2; 1.

REMBL; X79493; G50071; HOMEOBOX_2; 1.

RE
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                                                                                                                                                                                                                              EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; FRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; PISUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-OREGON R; TISSUE-EMBRYO, AND IMAGINAL DISKS;
MEDLINE; 9433757.

MULLDORF U., KLOTER U., GEHRING W.J.;
HOMOLOGY Of the eyeless gene of Drosophila to the Small eye gene in mice and Aniridia in humans.";
SCIENCE 265:785-789(1994).

-I-FUNCTION: INVOLVED IN EXE MORPHOGENESIS.
-I-TISSUE SPECIFICITY: EXPRESSION IS CONFINED TO THE EYE IMAGINAL DISCS, PARTS OF THE BRAIN, THE VENTRAL GANGLION AND THE SALIVARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 1.90e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 92; DB 5; Length 857;
Pred. No. 1.90e+00;
19; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-PERICARP;
RODRIGUEZ-CONCEPCION M., PEREZ-GARCIA A., BELTRAN J.;
SUBMITIED (VOL1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
BENBL; 2678873; E208986; -.
SEQUENCE 106 AA; 11828 MW; A45AD924 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 PRELIMINARY; PRT; 857 AA. 018381 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-3781; 01-
                                          01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
POLANG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
POLLINE- AND LEWCLINE-RICH PROTEIN.
PISUM SATIVUM (GARDEN PEA).
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    01-NOV-1996 (TREMBLREL. 01, CREATED)
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ilarity 28.3%;
Conservative
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Best Local Similarity 61.9%;
Matches 13; Conservative
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411 4
857 AA;
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Best Local Similarity
Matches 15; Conserv
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SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIGURE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 97166212.

MEDLINE; 97166212.

PETERSEN C.M., NIELSEN M.S., NYKJAER A., JACOBSEN L., TOMMERUP N., RASMUSSEN H.H., ROIGAARD H., GLIEMANN J., MADSEN P., MOESTRUP S.K.; "Molecular identification of a novel candidate sorting receptor purified from human brain by receptor-associated protein affinity chromatography."

J. BIOL. CHEM. 272:3599-3605(1997).

EMBL; X98248; E246784; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 LLDGGMPQMAGHLLDNMKLRGVAPQDLRLILLSHAHADHAGPVAELKRRTGAHVAANA 129
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                                                                                                                                                                                                                                                                           STENOTROPHOMONAS MALTOPHILIA.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; LYSOBACTERALES;
XANTHOMONAS GROUP; STENOTROPHOMONAS.
                     Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
L-1 METALLO-BETA-LACTAMASE.
9B37947D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                STRAIN=GN12873;
SANGCHAGRIN F., DUFRESNE J., LEVESQUE R.C.;
SAUBMITTED (JUN-197) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF010282; G2723332;
                                                                                                                                                                  JUN-1998 (TREMBLREL. 06, CREATED)
JUN-1998 (TREMBLEL. 07, LAST SEQUENCE UPDATE)
AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
METALLO-BETA-LACTAMASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 90; DB 2; Ler
Pred. No. 3.32e+00;
18; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 90; DB 4; L. Pred. No. 3.32e+00; 5; Mismatches 6
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D2E351B9 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 33 PC
34 290 L
290 AA; 30806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92408 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 10.0%;
Local Similarity 29.3%;
Les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY 1997 (TREMBLREL. 03, 01-MAY-1997 (TREMBLREL. 03, 01-NOV-1998 (TREMBLREL. 08, SORILLIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 10.0%;
Local Similarity 53.3%;
nes 16; Conservative
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                                                                                                                          PRELIMINARY;
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                                                                                                                                                               01-JUN-1998 (
01-JUN-1998 (
01-AUG-1998 (
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· 在我的,我们的人们的人们的人们的人们的人们的,我们们的人们的人们的人们的人们的人们的人们的人们的人们的人们的人们的人名 医克勒特氏征 医克勒氏征 医克勒氏征 医克勒氏征 医克勒特氏征 医克勒氏征 医克勒氏征检查检验检检验检检验检检验检检验检检检检检检检检检检检检检检检检检检检检检检		*****
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Aug 20 21:10:43 1999; MasPar time 4.50 Seconds 249.097 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-938-548B-9 (1-28) from US08938548B.pep 201 1 RPGPPGLQGRLQALGANGNHAAGILIM 28

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 15

122810 segs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Mean 30.698; Variance 52.943; scale 0.580 Statistics:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.77e+00	1.77e+00	1.77e+00	2.52e+00	5.02e+00	5.02e+00	5.02e+00	5.02e+00	7.06e+00	7.06e+00	7.06e+00	7.06e+00	7.06e+00	7.06e+00	9.90e+00	9.90e+00	9.90e+00	1.38e+01	1.38e+01	1.38e+01	1.92e + 01	1.92e+01	1.92e+01
	Description	hypothetical protein		superoxide dismutase	hypothetical protein	mALDP protein - mouse	membrane protein ydbH	hypothetical protein	NuMA protein - human	hypothetical protein	-	transcription initiat	transcription initiat	transcription initiat		deoxyuridine 5-tripho	hypothetical protein		probable ABC transpor	adenylate cyclase (EC	fatty-acid synthase (hypothetical protein	proteinase 3 (EC 3.4.	hypothetical protein
	ID	T00987	B41654	A41654	T02269	S47044	H64888	T00730	S23647	E69913	S11712	S41307	JN0443	JN0445	A55152	D69081	S49183	S19248	T02644	A33988	G01880	S25618	PRHU3	S51155
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onero	Match	35.3	35.3	35.3	34.8	33.8	33.8	33.8	33.8	33.3	33.3	33.3	33.3	33.3	33.3	32.8	32.8	32.8	32.3	32.3	32.3	31.8	31.8	31.8
	Score	7.1	71	71	70	68	68	68	68	29	29	67	29	67	29	99	99	99	65	65	65	64	64	64
Pecult	No.	Н	7	9	4	S	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.92e+01 1.92e+01 1.92e+01 1.92e+01 1.92e+01 1.92e+01 2.67e+01 2.67e+01 2.67e+01 3.68e+01 3.68e+01 3.68e+01 3.68e+01 3.68e+01 3.68e+01	ana use-ear change .L.; Venter, mic	Gaps 0; or -
hrpE protein - Pseudo protein-tyrosine-phos protein tyrosine-phos sulfite reductase (fe probable epidermal ce robable epidermal ce voR! protein - yeast hypothetical protein ribosomal protein 52, hypothetical protein hypothetical protein hypothetical protein collagen collage receptor - factor vIII-associate transcription initiat transcription initiat collagen alpha 1(XVIII hypothetical protein mitogen-activated procollagen alpha 1(XVIII mitogen-activated procollagen alpha 1(XVIII collagen alpha 1(XVIII collagen alpha 2(IV)	S 20.21 - Arabidopsis thali thaliana #common_name mc vision 12-Feb-1999 #text_ Ketchum, K.A.; Crosby, M S.M.; Kaul, S.; Mason, T. M.D.; Somerville, C.R.; ta Library, April 1998 omosome II BAC T9022 genc ated from GB/EMBL/DDBJ ID:g2739359; PID:g2739379	DB 2; Length 145; 1.77e+00; natches 6; Indels 0; 1.15.1.1) (Cu-Zn) precur nzae parainfluenzae parainfluenzae 71sion 12-Jun-1992 #text_ R:; Loynds, B.M.
S61858 A46101 BA6101 BA6101 S27812 A43917 S64616 S16463 A42115 B4433 C64835 S77523 S77523 S41221 A42832 S61292 A42832 S61292 A42833 C6483 C6483	ALIGNMENT Type complet Protein T9J Arabidopsis *Arabidopsis D.; Lin, X.; C.; Sykes, A.R.; Adams Othe EMBL Da thaliana chr nary; translac002505; N 78/2; 123/2 #molecular-	Score Pred. 8; 8; 5 138 c 24 c 24 c comp utase amoninf emoninf quence ngford
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                                                                                                                                                   Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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hypothetical protein F22013.25 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain transmembrane #status predicted #label TM01
#length 879 #molecular-weight 96834 #checksum 5911
                 H64888 #type complete
membrane protein ydbH - Escherichia coli
#formal_name Escherichia coli
12-Sep-1997_#sequence_revision 17-Sep-1997 #text_change
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#length 1015 #molecular-weight 111751 #checksum 6299
                                                                                                                                                                                                                                                 #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12
#cross-references MUID:97426617
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##slatus
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Pred. No. 5.02e+00;
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Pred. No.
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Best Local Similarity 50.0%;
Matches 13; Conservative
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Best Local Similarity 45.8%;
Matches 11; Conservative
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Alloni, G.; Acevedo, V.; Bortect, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Broursier, L.; Brans, Bolotin, A.; Borchert, S.; Bolotin, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brounilet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.; Brlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrart, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Haicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Barro, W.; Medique, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Porteclel, D.; Porwolik, S.; Park, S.; Schroeter, R.; Scoffone, F.; Scklyuchi, J.; Takemaru, K.; Takenchi, M.; Tamakoshi, A.; Tanaka, T.; Takemaru, K.; Takenchi, M.; Tanakoshi, A.; Tanaka, T.; Takemaru, K.; Takenchi, M.; Tanakoshi, A.; Tanaka, T.; Takemaru, K.; Vandelbri, M.; Tanakoshi, A.; Tanaka, T.; Wandhets, P.; Wedler, F.; Vasannoto, H.; Vanambutt, R.; Wedler, A.; Yasannoto, H.; Vaname, K.; Yata, K.; Yata, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
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J. Cell Biol. (1992) 116:1303-1317
NuMA: an unusually long coiled-coil related protein in the
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hypothetical protein yonC - Bacillus subtilis
#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
24-Sep-1998
$23647  #type complete

NuMA protein - human

#formal_name Homo sapiens #common_name man

19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
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Best Local Similarity 50.0%;
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Search completed: Fri Aug 20 21:10:58 1999 Job time : 15 secs.
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Best Local Similarity 50.0%;
Matches 9; Conservative
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10 RLQRLLQANGNHAAG 24
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characterstic of principal sigma factors.
#cross-references MUID:93083996
                                                                     #superfamily Streptomyces transcription initiation factor
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#formal_name Streptomyces aureofaciens
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
17-Mar-1999
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PASI protein - yeast (Pichia pastoris)
#formal_name pichia pastoris
06-Jan-1995_#sequence_revision 06-Jan-1995 #text_change
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J. Cell Biol. (1994) 127:1259-1273
Role of the PASI gene of Pichia pastoris in peroxisome
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#length 525 #molecular-weight 57204 #checksum 9676
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#length 528 #molecular-weight 57598 #checksum 7360
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Pred. No. 7.06e+00;
9; Mismatches 5; Indels
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##residues 1-528 ##label KOR
##cross-references GB:M90412; NID:g153308; PID:g153309
##residues 1-525 ##label KOR
##cross-references GB:M90411; NID:g153305; PID:g153306
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Gene (1992) 122:63-70
                                                                                                                                                                                                             Score 67; DB 2; Lo
Pred. No. 7.06e+00;
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#accession A55152
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Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.; Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P.; Lumm, W.; Pothler, B.; Qlu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Caruso, A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.; McDougall, S.; Safer, G.; Goyal, A.; Pietrokovski, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, ##cross-references GB:AE000920; GB:AE000666; NID:g2622729; PID:g2622730 ##experimental_source strain Delta H D69081 #type complete
deoxyuridine 5-triphosphate nucleotidohydrolase related
protein - Methanobacterium thermoautotrophicum (strain
Delta H) #formal_name Methanobacterium thermoautotrophicum
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Jun-1998 #checksum 2540 #superfamily FtsH/SEC18/CDC48-type ATP-binding domain homology ATP; P-loop; peroxisome biogenesis #region nucleotide-binding motif A (P-loop)\
#domain FtsH/SEC18/CDC48-type ATP-binding domain
homology #label VATP\
#region nucleotide-binding motif A (P-loop)
#length 1157 #molecular-weight 126983 #checksum 254C J. Bacteriol. (1997) 179:7135-7155 Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis ö preliminary; nucleic acid sequence not shown; #length 150 #molecular-weight 16996 #checksum Score 67; DB 2; Length 1157; Pred. No. 7.06e+00; 4; Mismatches 2; Indels Length 150; Score 66; DB 2; Le Pred. No. 9.90e+00; 5; Mismatches 4 translation not shown comparative genomics. 1-150 ##label MTH #cross-references MUID:98037514 #accession D69081 J.; Reeve, J.N. preliminary e_type DNA Query Match 33.3%; Best Local Similarity 60.0%; Matches 9; Conservative 1072 KLEHLYQGNGNHAEG 1086

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4; Indels